

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2004, 11:05:26 ; Search time 25 Seconds
(without alignments)

541.530 Million cell updates/sec

Title: US-10-063-735-128

Perfect score: 1337

Sequence: 1 MARGMERWRDLALVTGAS.....STPAHIQIGIQMPTEQVT 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	331.5	24.6	248	1	YDFG_SALTY
2	329.5	24.6	248	1	YDFG_ECOLI
3	317.5	23.7	252	1	YDFG_HAEIN
4	314.5	23.5	238	1	YDXD_BACSU
5	295	22.1	251	1	Y484_MYCTU
6	293	21.9	267	1	YMW1_YEAST
7	287.5	21.5	245	1	NDQG_RHIS3
8	278.5	20.8	249	1	SDH_AGRU
9	278	20.8	259	1	YQJQ_BACSU
10	275.5	20.6	249	1	SDH_AGRTS
11	271.5	20.3	246	1	FABG_BACSU
12	269	20.1	246	1	FABG_THENA
13	269	20.1	248	1	Y432_LISMO
14	269	20.1	248	1	Y452_LISIN
15	269	20.1	260	1	NDG4_BOVIN
16	268.5	20.1	245	1	NODG_RHIME
17	267.5	20.0	320	1	FABG_CUPLA
18	256.5	19.3	244	1	FABG_VIBCH
19	251	18.8	260	1	DHS4_RABIT
20	249.5	18.7	261	1	ACT3_STRCO
21	248	18.5	260	1	DHS4_PIG
22	246	18.4	260	1	DHS4_HUMAN
23	245.5	18.4	244	1	FABG_VIBHA
24	244	18.2	260	1	DHS4_MOUSE
25	243	18.2	261	1	DHG2_BACME
26	239	17.9	247	1	FAG1_SYNY3
27	239	17.9	260	1	DHS4_RAT
28	238.5	17.8	244	1	FABG_EUCAL
29	238.5	17.8	244	1	FABG_EUCAP
30	238	17.8	248	1	Y4EK_RHISN
31	237.5	17.8	272	1	DHK1_STRVN
32	237.5	17.8	319	1	FABG_ARATH
33	237.5	17.8	336	1	T82_MAIZE

34 236.5 17.7 244 1 CBR2_MOUSE
35 236 17.7 246 1 PHBB_CHRVI
36 236 17.7 249 1 BA71_EUBSP
37 235.5 17.6 253 1 Y945_MYCTU
38 234.5 17.5 244 1 CBR2_PIG
39 234 17.5 256 1 BUDC_KLEPN
40 232 17.4 248 1 PHAB_ACISP
41 230.5 17.2 248 1 FABG_AQUAE
42 230.5 17.2 287 1 HETN_ANASP
43 229 17.1 261 1 DHGA_BACME
44 229 17.1 271 1 SDR1_PICAB
45 228.5 17.1 278 1 Y4LA_RHISN

P08074 mus musculus
P45375 chromatium
P07914 eubacterium
P71564 mycobacteri
Q29529 sus scrofa
Q48436 klebsiella
P50203 acinetobact
O67610 aquifex aeo
P37694 anabaena sp
P10528 bacillus me
Q08632 picea abies
P55541 rhizobium s

ALIGNMENTS

RESULT 1
YDFG_SALTY STANDARD; PRT; 248 AA.
AC P40864;
DT 01-FEB-1995 (Rel. 31, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical oxidoreductase ydfg (EC 1.-.-.-).
GN YDFG OR STM1511 OR STY1550 OR T1432.
OS Salmonella typhimurium, and
OC Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602, 601;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2.";
RL Nature 413:852-856(2001).
RN [2]
RP SEQUENCE OF 1-97 FROM N.A.
RC SPECIES=S.typhimurium;
RX MEDLINE=92165738; PubMed=1537804;
RA Miller C.G., Hamilton S.;
RT "Cloning and nucleotide sequence of the Salmonella typhimurium dcp
gene encoding dipeptidyl carboxypeptidase.";
RL J. Bacteriol. 174:1626-1630(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagels K.,
RA Krogh A., Larsen T.N., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2

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RT and CTL8.";
RL J. Bacteriol. 185:2330-2337(2003).
RN [5]
RP IDENTIFICATION.
RC SPECIES=S.typhimurium;
RX MEDLINE=95004589; PubMed=7920643;
RA Robison K., Gilbert W., Church G.M.;
RT "Large scale bacterial gene discovery by similarity search.";
RL Nat. Genet. 7:205-214(1994).
CC CC -|- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY. STRONG, TO OTHER BACTERIAL HOMOLOGS.
CC
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CC -----
CC EMBL; AE008766; AAL20430.1; -;
CC EMBL; M84575; -; NOT ANNOTATED_CDS.
CC EMBL; AL627270; CAD01802.1; -;
CC EMBL; AE016838; AAO69074.1; -;
CC DR StyGene; SG10499; ydfG.
CC DR InterPro; IPR002198; ADH_short.
CC Pfam; PF00106; adh_short; 1.
CC DR PRINTS; PR00080; SDRFAMILY.
CC DR PROSITE; PS00061; ADH_SHORT; 1.
CC KW Hypothetical protein; Oxidoreductase; Complete proteome.
FT NP_BIND 4 28 NAD OR NADP (BY SIMILARITY).
FT ACT_SITE 147 147 BY SIMILARITY.
FT CONFLICT 56 70 NRRAIEEMWASLPA -> QPRGHRDDGLSAS (IN
FT REF. 2).
SQ SEQUENCE 248 AA; 27043 MW; A99FEC9188EFC8E4 CRC64;
Query Match 24.8%; Score 331.5; DB 1; Length 248;
Best Local Similarity 35.1%; Pred. No. 8.3e-21;
Matches 87; Conservative 36; Mismatches 111; Indels 13; Gaps 6;
QY 13 LALVTGASGGIGAAVARALVQGLKVGVCARTVGNIEELAAECKSAGYEGTLIPYRCDLS 72
Db : |||||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
QY 2 IVLVGTAGTAGECTARRFVGHKVIATGRHRERLQALKDELGE-----NVLTQLDVR 56
Db : |||||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
QY 73 NEEDILSFSAIRSHSGVDICINAGLARP-DTLLSGTSGWKDMFNVLALSICITRE 131
Db |||||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
QY 57 NRAAIEEMWASLPAQMRDIDLVLNNAGLALGLEPAHKASVEDWETMTDNNKGLTYMTRA 116
Db |||||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
QY 132 AYQSMKERNVDDGHIININSMGHRVPLSVTHFYSAKYAVTALTEGLROELREAQTHI 191
Db |||||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
QY 117 VLPGNVERN--RGHIINIGSTAGS--WPYAGNVYCATKAFVQPSLNLRITDLH--GTAV 170
Db |||||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
QY 192 RATCISPGVW-ETQAFKLHDKDPEKAAATYEQMKCLPEDVAEAVIYVLSTPAHIQIGD 250
Db |||||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
QY 171 RVTDIEPLGVGGTEPSSVRFGDDKAGKAGTYENTALTPEITAEVWVWVATLPAHVNIPT 230
Db |||||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
QY 251 IQMRPTEQ 258
Db : |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
QY 231 VEMMPVTQ 238
Db : |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
RESULT 2
YDFG_ECOLI
ID YDFG_ECOLI STANDARD; PRT; 248 AA.
AC P39831; P77149; P78161; P78162;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable oxidoreductase ydfG (EC 1.-.-.-).
GN YDFG OR B1539.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.

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OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M.,
RA Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T.,
RA Motomura K., Nakade S., Nakamura Y., Nishimoto H., Nishio Y.,
RA Oshima T., Saito N., Sampei G., Seki Y., Sivasubram S.,
RA Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C.,
RA Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 1-182 FROM N.A.
RC STRAIN=K12;
RX MEDLINE=94042903; PubMed=8226676;
RA Henrich B., Becker S., Schroeder U., Plapp R.;
RT "dcp gene of Escherichia coli: Cloning, sequencing, transcript
RT mapping, and characterization of the gene product.";
RL J. Bacteriol. 175:7290-7300(1993).
RN [4]
RP IDENTIFICATION.
RX MEDLINE=95075659; PubMed=7984428;
RA Borodovsky M., Rudd K.E., Koonin E.V.;
RT "Intrinsic and extrinsic approaches for detecting genes in a
RT bacterial genome.";
RL Nucleic Acids Res. 22:4756-4767(1994).
RN [5]
RP SEQUENCE OF 1-12.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RT in the genome of Escherichia coli K-12.";
RL Electrophoresis 18:1259-1313(1997).
CC CC -|- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY. STRONG, TO OTHER BACTERIAL HOMOLOGS.
CC -|- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 58.
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CC -----
CC EMBL; AE000251; AAC74612.1; -;
CC EMBL; D90796; BAA15229.1; -;
CC EMBL; D90797; BAA15241.1; -;
CC EMBL; D90798; BAA15245.1; -;
CC EMBL; X57947; -; NOT ANNOTATED_CDS.
CC PIR; P64908; F64908.
CC HSSP; P14061; 1FDU.
CC Ecogene; EG12345; ydfG.
CC InterPro; IPR002198; ADH_short.
CC Pfam; PF00106; adh_short; 1.
CC PRINTS; PR00080; SDRFAMILY.
CC PROSITE; PS00061; ADH_SHORT; 1.

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RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mael C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowaka A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takenaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Toato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler E., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.",
RL Nature 390:249-256(1997).
RN [3]
RP SEQUENCE OF 62-238 FROM N.A.
RC STRAIN=168;
RX MEDLINE=88040469; PubMed=3118336;
RA Carrigan C.M., Haarsma J.A., Smith M.T., Wake R.G.;
RT "Sequence features of the replication terminus of the Bacillus
RT subtilis chromosome";
RL Nucleic Acids Res. 15:8501-8509(1987).
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
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CC -----
DR EMBL; X06168; CA229533.1; -;
DR EMBL; Z99114; CAB13743.1; -;
DR PIR; D69930; D69930.
DR HSSP; O70351; 1E3S.
DR Subtilist; BG11048; yoxD.
DR InterPro; IPR002198; ADH short.
DR Pfam; PF00106; adh short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
DR Hypothetical protein; Oxidoreductase; Complete proteome.
FT NP BIND 10 34 NAD OR NADP (BY SIMILARITY).
FT ACT SITE 155 155 BY SIMILARITY.
SQ SEQUENCE 238 AA; 25299 MW; 9CC7A8D1204DF248 CRC64;
Query Match 23.5%; Score 314.5; DB 1; Length 238;
Best Local Similarity 32.7%; Pred. No. 2.1e-19;
Matches 80; Conservative 50; Mismatches 96; Indels 19; Gaps 6;
QY 6 MERWEDRLALVTGASGGIGAAVARALVQGLKVVGCARTVGNIEELAAECKSAGYPTLI 65
Db 1 MQLSQHTALITGGRGIGRATALLAKEGVNIGIGRTSANVEKVAEVEALGVKAAPA 60
QY 66 PYRCLDSNEEDILSMFSAIRSHQSGVDICINNAGLARPTLLSGTSGMKDMFNVLAL 125
Db 61 --AADVKDAQVNOAQAQVKEQLGDIDILINNAGISKFGGLDLSADEWENIIQVNLGV 118
QY 126 SCTTEAATQSMKERNVDGHIININSMGHRVLPVSVTHFYSATKYAVTALTEGLRQELR 185
Db 119 YHVTVRAVLPEMTERKA--GDIINISITAGQR--GAAVTSAVSASFVLGITESLMQEVYR 174
QY 186 EAQTHIRATCTSPGVVETQFAFKLH--DKDPKAAATVEQMKCLKPEQVAAVIVVLSTP 243
Db 175 --KXNIRVSALTPTSVADMSIELNLTGNPEKV-----MQPEDLAETVVAQLKLD 223
QY 244 AHIQI 248

Db 224 PRIFI 228
RESULT 5
Y484 MYCTU STANDARD; PRT; 251 AA.
AC Q11150;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Putative oxidoreductase RV0484C/MT0502 (EC 1.-.-.-).
GN RV0484C OR MT0502 OR MTCY20C9.10C.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon K.V., Eiglmeier K., Gas S., Barry C.B. III, Tekai F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey B.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Bisher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains";
RL J. Bacteriol. 184:5479-5490(2002).
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY. STRONG, TO BACTERIAL YDFG HOMOLOGS.
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CC -----
DR EMBL; Z77162; CAB00945.1; -;
DR EMBL; AE006951; AAK44725.1; -;
DR PIR; G70743; G70743.
DR HSSP; F14061; IFDU.
DR TIGR; MT0502; -;
DR Tuberculist; RV0484C; -;
DR InterPro; IPR002198; ADH short.
DR Pfam; PF00106; adh short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; FALSE NEG.
KW Hypothetical protein; Oxidoreductase; Complete proteome.
FT NP BIND 12 36 NAD OR NADP (BY SIMILARITY).
FT ACT SITE 149 149 BY SIMILARITY.
SQ SEQUENCE 251 AA; 26416 MW; 6F3956B95DB92BA2 CRC64;
Query Match 22.1%; Score 295; DB 1; Length 251;
Best Local Similarity 34.3%; Pred. No. 1e-17;
Matches 87; Conservative 43; Mismatches 102; Indels 22; Gaps 8;

RESULT 6	YMW71 YEAST	STANDARD;	PRT;	267 AA.
ID	YMW71 YEAST			
AC	Q05016;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Hypothetical oxidoreductase in MRPL44-MTF1 intergenic region			
DE	(EC 1.-.-.-.-)			
GN	YMR226C OR YM9959.08C.			
OS	Saccharomyces cerevisiae (Baker's yeast).			
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
OC	Saccharomycetales; Saccharomycetaceae; Saccharomycetes.			
NCBI_TaxID=4932;				
GN	[1]			
RE	SEQUENCE FROM N.A.			
RC	STRAIN=S288C / AB972;			
RX	MEDLINE=97313268; PubMed=3169872;			
RA	Bowman S., Church C.M., Badcock K., Brown D., Chillingworth T.,			
RA	Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,			
RA	Jagels K., Iye G., Moule S., Odell C., Pearson D., Rajandream M.A.,			
RA	Rice P., Skelton J., Walsh S., Whitehead S., Barrell B.G.;			
RT	"The nucleotide sequence of Saccharomyces cerevisiae chromosome			
RT	XIII.,"			
RL	Nature 387:90-93(1997).			
CC	-1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES			
CC	(SDR) FAMILY. STRONG, TO BACTERIAL YDFG HOMOLOGS.			
CC	-----			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
CC	EMBL; Z49939; CAA90197.1; --			
DR	PIR; S57593; S57593.			
DR	HSSP; P14061; IFDU.			
DR	GermOnline; 142901; --			
DR	SGD; S0004839; YMR226C.			
DR	InterPro; IPR002198; ADH_short.			
DR	Pfam; PF00106; adh_short; 1.			
DR	PRINTS; PR00080; SDRFAMILY.			
DR	PROSITE; PS00061; ADH_SHORT; 1.			
KW	Hypothetical protein; Oxidoreductase.			
FT	NP BIND 17 44 NAD OR NADP (BY SIMILARITY).			
FT	ACT SITE 168 168 BY SIMILARITY.			
FT	SEQUENCE 267 AA; 29158 MW; 77FCD713F724A9D7 CRC64;			
CC	-----			
CC	Query Match 21.9%; Score 293; DB 1; Length 267;			
CC	Best Local Similarity 30.8%; Pred. No. 1.6e-17;			

```

Db 7 KALVTGASGGIGEAIRALRVLAHQ-AIVLHGTRVEKLETLAAE---LGDRVKLP--AN 60
Qy 71 LSNBEDILSMFAIRSOHSGVDICINNAGLARPDTLLSGTSGWKDMFNVNVLALSICTR 130
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 LSNRDEVKALQKAEDLEGVDILVNNAGITKGLFVRMSDADWDVLEVNLTAVFRLTR 120
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 131 EAYQSMKERNVDDGHIININSMGHRVLPVLSVTHFYSAKYAVTALTSLGRLQELBEAQTH 190
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 ELTHPMRMR--HGRINITSVVGVTGNPGQTN--YCASKAGMIGFSKLAQEI--ATRN 174
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 191 IRATCISPGVVEVTOFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIVLSTPA 244
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 175 ITVNCVAFGFIESAMTKLNDKQKALMAIPTREMGTSVEVASAVIASNEA 228
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
SDH_AGRU
ID SDH_AGRU STANDARD; PRT; 249 AA.
AC Q9KWN1;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE Serine 3-dehydrogenase (EC 1.1.1.276).
GN SDH.
OS Agrobacterium tumefaciens.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=358;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR1600;
RX MEDLINE=22087129; PubMed=12092831;
RA Fujisawa H., Nagata S., Chowdhury E.K., Matsumoto M., Misono H.;
RT "Cloning and sequencing of the serine dehydrogenase gene from
RT Agrobacterium tumefaciens.";
RL Biosci. Biotechnol. Biochem. 66:1137-1139(2002).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=97179806; PubMed=9028042;
RA Chowdhury E.K., Higuchi K., Nagata S., Misono H.;
RA "A novel NADP(+)-dependent serine dehydrogenase from Agrobacterium
RT tumefaciens.";
RL Biosci. Biotechnol. Biochem. 61:152-157(1997).
CC -!- FUNCTION: Catalyzes the oxidation of the hydroxyl group of serine
CC to form 2-aminomalonate semialdehyde which is spontaneously
CC converted into 2-aminoacetaldehyde and CO(2). Also acts on D-
CC serine, L-glycerate, D-glycerate and 2-methyl-DL-serine. Does not
CC act on O-methyl-DL-serine and L-threonine.
CC -!- CATALYTIC ACTIVITY: L-serine + NADP(+) = 2-aminomalonate
CC semialdehyde + NADPH.
CC -!- SUBUNIT: Homotetramer.
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
-----
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-----
DR EMBL; AB032242; BAB07807.1; -.
DR PIR; JC7857; JC7857.
DR HSSP; Pf4061; IFDU.
DR InterPro; IPR002198; ADH short.
DR Pfam; PF00106; adh short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR TIGRFAMs; TIGR01831; fabg rel; 1.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NADP.
FT NP_BIND 6 30 NADP (BY SIMILARITY).
FT ACT_SITE 148 148 BY SIMILARITY.

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SQ SEQUENCE 249 AA; 26745 MW; 5DCE3C404C950BDA CRC64;
Query Match 20.8%; Score 278.5; DB 1; Length 249;
Best Local Similarity 29.7%; Pred. No. 2.5e-16;
Matches 74; Conservative 45; Mismatches 109; Indels 21; Gaps 7;
Qy 15 LVTGASGGIGEAIRALRVLAHQ-AIVLHGTRVEKLETLAAE---LGDRVKLP--AN 74
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 LITGASGGIGEAIRALRVLAHQ-AIVLHGTRVEKLETLAAE---LGDRVKLP--AN 60
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 75 EDILSMFAIRSOHSGVDICINNAGL-----RPTLLSGTSGWKDMFNVNVLALSICT 129
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 EATKALAGLPGDFRIDILVNNAGLALGTAPAPQVPL-----KQQTWVDNITGLNVT 116
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 130 REAYQSMKERNVDDGHIININSMGHRVLPVLSVTHFYSAKYAVTALTSLGRLQELBEAQTH 189
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 117 HHLPLTLIERK---GIVINLSSVAH--YPLVGGNVYGGTKAFRLQFSLGRSDIHL--GK 169
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 190 HIRATCISPGVVEVTOFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIVLSTPAHQIG 249
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 170 GVRVTSIEPGMCETEFTLVRTGGQASDNLYKGNVPTADDIANTIHVASQPKHININ 229
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 250 DIQMRPTEQ 258
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 230 SLELMPVQ 238
| | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
YQJQ_BACSU
ID YQJQ_BACSU STANDARD; PRT; 259 AA.
AC P54554;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical oxidoreductase yqjQ (EC 1.-.-.-).
GN YQJQ OR BSU23780.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / JH642;
RX MEDLINE=97124195; PubMed=8969508;
RA Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
RA Kobayashi Y.;
RT "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of
RT the Bacillus subtilis genome containing the skin element and many
RT sporulation genes.";
RL Microbiology 142:3103-3111(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Boursier M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriello R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerston I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guiseppe G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,

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QY 190 HIRATCISPGVVETQFAFKLHDKDEKAAATYEQMKCLKPEDVAEAVIYVLSTPAHIQIG 249
 Db 170 GVRVTSIEPGMCETEFTLVRTGNGQASDNLKYGVPNTADDIANTYIYVWASQPKHIN 229
 QY 250 DIQMRPTQ 258
 Db 230 SLELMPVQ 238
 RESULT 11
 ID _FABG_BACSU STANDARD; PRT; 246 AA.
 AC P51831; 031733;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
 DE acyl carrier protein reductase).
 GN FABG OR BSU15910.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=96326321; PubMed=8759840;
 RA Morbidoni H.R., de Mendoza D., Cronan J.B. Jr.;
 RT "Bacillus subtilis acyl carrier protein is encoded in a cluster of
 RT lipid biosynthesis genes."
 RL J. Bacteriol. 178:4794-4800(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Bruillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
 RA Enitan K.D., Errington J., Fabret C., Ferrati E., Foulger D.,
 RA Fritz G., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
 RA Guisepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis.";
 RL Nature 390:249-256(1997).
 RN [3]
 RP SEQUENCE OF 1-172 FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98195738; PubMed=9534248;
 RA Foulger D., Errington J.;
 RT "A 28 kbp segment from the spoVM region of the Bacillus subtilis 168
 RT genome.";

Microbiology 144:801-805(1998).
 RL [4]
 RN SEQUENCE OF 230-246 FROM N.A.
 RP STRAIN=168;
 RA Oguro A., Kakeshita H., Takamatsu H., Nakamura K., Yanane K.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 CC 1- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] +
 CC NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
 CC 1- PATHWAY: Fatty acid biosynthesis pathway; first reduction step.
 CC 1- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
 CC (SDR) family.
 CC -----
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 CC -----
 DR EMBL; U59433; AAC44307.1; -;
 DR EMBL; Z99112; CAB13464.1; -;
 DR EMBL; Y13937; CAA74250.1; -;
 DR EMBL; D64116; BAA10974.1; -;
 DR PIR; A69621; A69621.
 DR HSSP; Q12634; 1YBV.
 DR Subtilist; BG11535; fabg.
 DR InterPro; IPR002198; ADH_short.
 DR Pfam; PF00106; adh_short; 1.
 DR PRINTS; PR00080; SDRFAMILY.
 DR PROSITE; PS00061; ADH_SHORT; FALSE NEG.
 KW Fatty acid biosynthesis; Oxidoreductase; NADP; Complete proteome.
 FT NP_BIND 9 33 NADP (BY SIMILARITY).
 FT ACT_SITE 154 154 BY SIMILARITY.
 FT CONFLICT 23 23 D -> A (IN REF. 1).
 SQ SEQUENCE 246 AA; 26282 MW; C6A391167D3237DC CRC64;
 Query Match 20.3%; Score 271.5; DB 1; Length 246;
 Best Local Similarity 32.9%; Pred. No. 9.4e-16;
 Matches 82; Conservative 38; Mismatches 10; Indels 27; Gaps 10;
 QY 11 DRLAVTGASGGIGAAVARALVQGLKYVGCAITVGN---TEELAAECKSAGYPTGLIPY 67
 Db 4 DKTAIVTGASRGIGRSIALDLAKSGANVV--VNYSGNEAKANEVVDKSMGRKA--IAV 59
 QY 68 RCDLSNEEDILSMFSAIRSQHSQVDICINAGLARPDTLLSGSTSGWKDMFNVLALSI 127
 Db 60 KADVSNPEDVQNMKETLSVFSTIDILVNNAGITRDNLIMRMKEDWDVNNILKGVFN 119
 QY 128 CTRE-AYOSMKERNVDDGHHININSMGSHRVLPVLSVTHFYSAKYAVTALTEGLRQELRE 186
 Db 120 CTKAVTROMMKQRS---GRINVSIVGVSGNPGQAN--YVAAKAGVTLGTLKSSAKEL-- 172
 QY 187 AQTHIRATCISPGVVETQFAFKLHDKDEKAAATYEQMKCL-----KPEDVAEAVIYVL 240
 Db 173 ASRNTVNAIAPGGFISTDMTKL-AKVDQD-----EMLKQIPLARFGPSDVSSVVTFLA 226
 QY 241 STPAHIQIG 249
 Db 227 SEGARYMTG 235
 RESULT 12
 FABG_THEME
 ID _FABG_THEME STANDARD; PRT; 246 AA.
 AC Q9X248;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE 3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-
 DE acyl carrier protein reductase).
 OS Thermotoga maritima.

[illegible]

```

Db      122 AAVLPSTFAQKS-----GHIATSSVAGLKAYPGGAV--YGATKWAVRDLMEVLRME 171
QY      184 LREAQTHIRATCISGVVETQFAFKLHDKDPKAAATYEQMKCLKPEDVAEAVIIVLSTP 243
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      172 SAQEGTNRITVTIYPAAINTELLETITDKETEQGTNLYKQGVTPDRIASIVAYAIQDP 231
QY      244 AHIQIGDIQMRPTEQ 258
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      232 EDVNVNEFTVGTSQ 246

RESULT 14
Y452 LISIN
ID Y452 LISIN STANDARD; PRT; 248 AA.
AC Q92EK7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical oxidoreductase Lin0452 (EC 1.-.-.-).
GN Lin0452.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OC NCBI TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaeser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetoui F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fshiz H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Krest J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Coseart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -! SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
      (SDR) family.
CC
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CC
CC EMBL; AL596165; CAC95684.1; -.
CC F1R; AD1489; AD1489.
CC ListList; LIN00452; -.
CC InterPro; IPR002198; ADH_short.
CC Pfam; PF00106; adh_short; 1.
CC PRINTS; PR00080; SDRFAMILY.
CC PROSITE; PS00061; ADH_SHORT; 1.
KW Hypothetical protein; Oxidoreductase; Complete proteome.
FT NP BIND 9 33 NAD OR NADP (BY SIMILARITY).
FT ACT SITE 154 154 BY SIMILARITY.
SQ SEQUENCE 248 AA; 26808 MW; EAE7EB01F110306F CRC64;

Query Match 20.1%; Score 269; DB 1; Length 248;
Best Local Similarity 27.8%; Pred. No. 1.5e-15;
Matches 71; Conservative 50; Mismatches 116; Indels 18; Gaps 4;

QY 10 RDRALVTGASGGGAARALVQOGLKVVGARTVGNTERLAEACKSAGYPTGLIPYRC 69
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 KKKVLIITGASSGIGATAILAEKAKLVLAARVEKLEKIVQTIKASS--GEALFAKT 61
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 70 DLNSNEEDILMSFAIRSKQSGVDVICINNAGLAPDPTLLSGSTSGWKMDPNVNV-----L 123
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db      62 DVTKEDNKKLVLAIERYKVDALFLNAGIMPNSPLSALKDEDEWEQIDINIKGVNLGI 121
QY      124 ALSICTRAYOSMKERNVDDGHIININSMGSHRVLPISVTHFYSA TKYAVTALTGLRQE 183
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      122 AAVLPSTFAQKS-----GHIATSSVAGLKAYPGGAV--YGATKWAVRDLMEVLRME 171
QY      184 LREAQTHIRATCISGVVETQFAFKLHDKDPKAAATYEQMKCLKPEDVAEAVIIVLSTP 243
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      172 SAQEGTNRITVTIYPAAINTELLETITDKETEQGTNLYKQGVTPDRIASIVAYAIQDP 231
QY      244 AHIQIGDIQMRPTEQ 258
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      232 EDVNVNEFTVGTSQ 246

RESULT 15
DHS4 BOVIN
ID DHS4 BOVIN STANDARD; PRT; 260 AA.
AC Q8SPU8;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Dehydrogenase/reductase SDR family member 4 (EC 1.1.1.184) (NADPH-
DE dependent carbonyl reductase/NADP-retinol dehydrogenase) (CR) (PCHR)
DE (Peroxisomal short-chain alcohol dehydrogenase) (NADPH-dependent
DE retinol dehydrogenase/reductase) (NDRD).
GN DHS4 OR NDRD.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Wang G.L., Liu G.F., Du J., Xu X.L., Gasana V., Wang B., Zhu L.,
RA Huang D.Y.;
RT "Bos taurus NDRD mRNA for NADPH-dependent retinol
RT dehydrogenase/reductase.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: Reduces all-trans-retinal and 9-cis retinal. Can also
CC catalyze the oxidation of all-trans-retinol with NADP as co-
CC factor, but with much lower efficiency. Reduces alkyl phenyl
CC ketones and alpha-dicarbonyl compounds with aromatic rings, such
CC as pyrimidine-4-aldehyde, 3-benzoylpyridine, 4-benzoylpyridine,
CC menadione and 4-hexanoylpyridine. Has no activity towards
CC aliphatic aldehydes and ketones (By similarity).
CC -! CATALYTIC ACTIVITY: R-CHOH-R' + NADP(+) = R-CO-R' + NADPH.
CC -! SUBUNIT: Homotrimer (By similarity).
CC -! SUBCELLULAR LOCATION: Peroxisomal (By similarity).
CC -! MISCELLANEOUS: Inhibited by kaempferol, quercetin, genistein and
CC myristic acid (By similarity).
CC -! SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
      (SDR) family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF487454; AAL93248.1; -.
CC InterPro; IPR002198; ADH_short.
CC Pfam; PF00106; adh_short; 1.
CC PRINTS; PR00080; SDRFAMILY.
CC PROSITE; PS00061; ADH_SHORT; 1.
KW Oxidoreductase; NADP; Peroxisome.
FT NP BIND 18 42 NADP (BY SIMILARITY).
FT SITE 258 260 MICROBODY TARGETING SIGNAL.
SQ SEQUENCE 260 AA; 27385 MW; F76610B3EF128C3D CRC64;

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Query Match 20.1%; Score 269; DB 1; Length 260;
Best Local Similarity 31.2%; Pred. No. 1.6e-15;
Matches 81; Conservative 51; Mismatches 106; Indels 22; Gaps 10;

QY	1	MARPGRWR---	DRLALVTGASGGIGAAVARALVOOGLKVVCARTVGNIEELAAECKS	57
Db	1	MASCGMARRNPLDNKVALVTASTDGGTGFARRLAQDGAHVVSRRKQNVDRAVATLKG	60	
QY	58	AG--YPGTLIPYKCDLSNEEDILSMFSAIRSQHSQGVDCINNAGLARP--DTLLSGSTSG	113	
Db	61	EGLSVTGTV-----CHVGKAEDRRLVATAVKLGVDLILISNAVS-PFFGSLMDVPEEV	115	
QY	114	WKDMFNVNVLALSICTREAYQSMKERNVDDGHIININSMGHRVLPVSVTHFYSAKYAV	173	
Db	116	WDKILDVNVKATALLTKAVVPMAKRG--GGSIVIVSSIAAYS--PFPSLGPYNVSKTAL	171	
QY	174	TALTEGLRQELREAOQHIRATCISPGVETQFAFKLHDKDP---EKAATYEQMKCLKPE	230	
Db	172	LGLTKNALLEL--AESNVVNCLAPGLINTSFSLWE-DPARQESIKATFQIKRIGKPE	228	
QY	231	DVAEAVIYVLSTPAHIQGD	250	
Db	229	ECAGIVSFLCSEDAZYITGE	248	

Search completed: September 15, 2004, 11:26:35
Job time : 27 secs

B/a < K

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2004, 11:26:12 ; Search time 52 Seconds

(without alignments)
1603.448 Million cell updates/sec

Title: US-10-063-735-128

Perfect score: 1337

Sequence: 1 MARPGMERWDRDLALVTGAS.....STPAHIQIGDIQMRPTEQVT 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1337	100.0	260	9	US-09-796-089-1	Sequence 1, Appli
2	1337	100.0	260	12	US-10-206-915-378	Sequence 378, App
3	1337	100.0	260	12	US-10-199-670-378	Sequence 378, App
4	1337	100.0	260	12	US-10-201-858-378	Sequence 378, App
5	1337	100.0	260	12	US-10-205-890-378	Sequence 378, App
6	1337	100.0	260	12	US-10-208-024-378	Sequence 378, App
7	1337	100.0	260	12	US-10-201-853-378	Sequence 378, App
8	1337	100.0	260	12	US-10-063-745-128	Sequence 128, App
9	1337	100.0	260	12	US-10-063-512-128	Sequence 128, App
10	1337	100.0	260	12	US-10-063-513-128	Sequence 128, App
11	1337	100.0	260	12	US-10-063-515-128	Sequence 128, App
12	1337	100.0	260	12	US-10-063-549-128	Sequence 128, App
13	1337	100.0	260	12	US-10-063-569-128	Sequence 128, App
14	1337	100.0	260	12	US-10-063-551-128	Sequence 128, App
15	1337	100.0	260	12	US-10-174-581-378	Sequence 378, App

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16 1337 100.0 260 12 US-10-176-483-378 Sequence 378, App
17 1337 100.0 260 12 US-10-176-749-378 Sequence 378, App
18 1337 100.0 260 12 US-10-176-914-378 Sequence 378, App
19 1337 100.0 260 12 US-10-176-915-378 Sequence 378, App
20 1337 100.0 260 12 US-10-063-555-128 Sequence 128, App
21 1337 100.0 260 12 US-10-063-563-128 Sequence 128, App
22 1337 100.0 260 12 US-10-063-594-128 Sequence 128, App
23 1337 100.0 260 12 US-10-063-553-128 Sequence 128, App
24 1337 100.0 260 12 US-10-063-554-128 Sequence 128, App
25 1337 100.0 260 12 US-10-176-484-378 Sequence 378, App
26 1337 100.0 260 12 US-10-180-550-378 Sequence 378, App
27 1337 100.0 260 12 US-10-183-014-378 Sequence 378, App
28 1337 100.0 260 12 US-10-187-738-378 Sequence 378, App
29 1337 100.0 260 12 US-10-187-740-378 Sequence 378, App
30 1337 100.0 260 12 US-10-187-883-378 Sequence 378, App
31 1337 100.0 260 12 US-10-194-363-378 Sequence 378, App
32 1337 100.0 260 12 US-10-194-460-378 Sequence 378, App
33 1337 100.0 260 12 US-10-194-463-378 Sequence 378, App
34 1337 100.0 260 12 US-10-194-484-378 Sequence 378, App
35 1337 100.0 260 12 US-10-195-884-378 Sequence 378, App
36 1337 100.0 260 12 US-10-195-896-378 Sequence 378, App
37 1337 100.0 260 12 US-10-196-744-378 Sequence 378, App
38 1337 100.0 260 12 US-10-196-755-378 Sequence 378, App
39 1337 100.0 260 12 US-10-196-757-378 Sequence 378, App
40 1337 100.0 260 12 US-10-197-704-378 Sequence 378, App
41 1337 100.0 260 12 US-10-197-710-378 Sequence 378, App
42 1337 100.0 260 12 US-10-198-758-378 Sequence 378, App
43 1337 100.0 260 12 US-10-198-766-378 Sequence 378, App
44 1337 100.0 260 12 US-10-199-304-378 Sequence 378, App
45 1337 100.0 260 12 US-10-199-309-378 Sequence 378, App

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ALIGNMENTS

RESULT 1

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US-09-796-089-1
; Sequence 1, Application US/09796089
; Patent No. US20020010946A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 21612, 21615, 21620, 21676, 33756, No. US20020010946A1e1
; TITLE OF INVENTION: Human Alcohol Dehydrogenases
; FILE REFERENCE: 35800/208222
; CURRENT APPLICATION NUMBER: US/09/796,089
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US00/33873
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 09/464,039
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-089-1

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Query Match      100.0%; Score 1337; DB 9; Length 260;
Best Local Similarity 100.0%; Pred. No. 6 6e-132;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARPGMERWDRDLALVTGASGGIGAAVARALVQOGLKVGCARTVGNIEELAAECKSAGY 60
    |||||
Db 1 MARPGMERWDRDLALVTGASGGIGAAVARALVQOGLKVGCARTVGNIEELAAECKSAGY 60
    |||||

Qy 61 PGTLPYRCDLNNEEDILSMFSAIRSHSGVDICINNAGLARPDITLLSGSTSGKDMFNV 120
    |||||
Db 61 PGTLPYRCDLNNEEDILSMFSAIRSHSGVDICINNAGLARPDITLLSGSTSGKDMFNV 120
    |||||

Qy 121 NVLALSICTREAYQSMKERNVDDGHIININMSGHRVLPISVTHFYSATKYAVTALTEGL 180
    |||||
Db 121 NVLALSICTREAYQSMKERNVDDGHIININMSGHRVLPISVTHFYSATKYAVTALTEGL 180
    |||||

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Qy 181 ROELREAQTHIRATCISPGVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
 Db 181 ROELREAQTHIRATCISPGVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
 Qy 241 STPAHIQIGDIQMRPTEQVT 260
 Db 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 2

US-10-206-915-378
 ; Sequence 378, Application US/10206915
 ; Publication No. US20040029221A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3430R1C513
 ; CURRENT APPLICATION NUMBER: US/10/206,915
 ; CURRENT FILING DATE: 2002-07-26
 ; PRIOR APPLICATION NUMBER: 10/052586
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR FILING DATE: 1997-10-21
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR FILING DATE: 1997-10-28
 ; Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 378
 ; LENGTH: 260
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-206-915-378

Query Match 100.0%; Score 1337; DB 12; Length 260;
 Best Local Similarity 100.0%; Pred. No. 6.6e-132;
 Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MARGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAITVGNIEELAAECKSAGY 60
 Db 1 MARGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAITVGNIEELAAECKSAGY 60
 Qy 61 PGTLLIPYRCDLSNEEDILSMFSAIRSQHSQVDICINNAGLARPDITLLSGSTSGWKDMFNV 120
 Db 61 PGTLLIPYRCDLSNEEDILSMFSAIRSQHSQVDICINNAGLARPDITLLSGSTSGWKDMFNV 120
 Qy 121 NVLALSICTREAYQSMKERNVDDGHIININSMGHRVPLSVTHFYFSATKYAVTALTEGL 180

Db 121 NVLALSICTREAYQSMKERNVDDGHIININSMGHRVPLSVTHFYFSATKYAVTALTEGL 180
 Qy 181 ROELREAQTHIRATCISPGVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
 Db 181 ROELREAQTHIRATCISPGVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
 Qy 241 STPAHIQIGDIQMRPTEQVT 260
 Db 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 3

US-10-199-670-378
 ; Sequence 378, Application US/10199670
 ; Publication No. US20040033560A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3430R1C401
 ; CURRENT APPLICATION NUMBER: US/10/199,670
 ; CURRENT FILING DATE: 2002-07-19
 ; PRIOR APPLICATION NUMBER: 10/052586
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059266
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063120
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063121
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063486
 ; PRIOR FILING DATE: 1997-10-21
 ; PRIOR APPLICATION NUMBER: 60/063540
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063541
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063544
 ; PRIOR FILING DATE: 1997-10-28
 ; Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 378
 ; LENGTH: 260
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 US-10-199-670-378

Query Match 100.0%; Score 1337; DB 12; Length 260;
 Best Local Similarity 100.0%; Pred. No. 6.6e-132;
 Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 1 MARGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAITVGNIEELAAECKSAGY 60
 Qy 61 PGTLLIPYRCDLSNEEDILSMFSAIRSQHSQVDICINNAGLARPDITLLSGSTSGWKDMFNV 120
 Db 61 PGTLLIPYRCDLSNEEDILSMFSAIRSQHSQVDICINNAGLARPDITLLSGSTSGWKDMFNV 120
 Qy 121 NVLALSICTREAYQSMKERNVDDGHIININSMGHRVPLSVTHFYFSATKYAVTALTEGL 180

Db 121 NVLALSICTREAYOSMKERNVDDGHIININSMGSHRVLPLSVTHFYSA TKYAVTALTEGL 180
Qy 181 RQELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
Db 181 RQELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
Qy 241 STPAHIQIGDIQMRPTEQVT 260
Db 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 4

US-10-201-858-378
; Sequence 378, Application US/10201858
; Publication No. US20040038337A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C464
; CURRENT APPLICATION NUMBER: US/10/201,858
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 378
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-201-858-378

Query Match 100.0%; Score 1337; DB 12; Length 260;
Best Local Similarity 100.0%; Pred. No. 6.6e-132;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCARTVGNIEELAAECKSAGY 60
Db 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCARTVGNIEELAAECKSAGY 60
Qy 61 PGTLPYRCDLNSNEEDILSMFSAIRSQHSQVDICINNAGLARPTLLSGSTSGKDMFNV 120
Db 61 PGTLPYRCDLNSNEEDILSMFSAIRSQHSQVDICINNAGLARPTLLSGSTSGKDMFNV 120

Qy 121 NVLALSICTREAYOSMKERNVDDGHIININSMGSHRVLPLSVTHFYSA TKYAVTALTEGL 180
Db 121 NVLALSICTREAYOSMKERNVDDGHIININSMGSHRVLPLSVTHFYSA TKYAVTALTEGL 180
Qy 181 RQELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
Db 181 RQELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
Qy 241 STPAHIQIGDIQMRPTEQVT 260
Db 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 5

US-10-205-890-378
; Sequence 378, Application US/10205890
; Publication No. US20040048334A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C519
; CURRENT APPLICATION NUMBER: US/10/205,890
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 378
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-205-890-378

Query Match 100.0%; Score 1337; DB 12; Length 260;
Best Local Similarity 100.0%; Pred. No. 6.6e-132;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCARTVGNIEELAAECKSAGY 60
Db 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCARTVGNIEELAAECKSAGY 60
Qy 61 PGTLPYRCDLNSNEEDILSMFSAIRSQHSQVDICINNAGLARPTLLSGSTSGKDMFNV 120
Db 61 PGTLPYRCDLNSNEEDILSMFSAIRSQHSQVDICINNAGLARPTLLSGSTSGKDMFNV 120

Qy	121 NVLALSICTREAYQSMKERNVDDGHIININMSGHRVLPLSVTHFYFSATKYAVTALTEGL 180
Dd	121 NVLALSICTREAYQSMKERNVDDGHIININMSGHRVLPLSVTHFYFSATKYAVTALTEGL 180
Qy	181 RQLREACQTHIRATCISPGVVETQFAFKLDKDPKAAATYEQMKCLKPEDVAEAVIYVL 240
Dd	181 RQLREACQTHIRATCISPGVVETQFAFKLDKDPKAAATYEQMKCLKPEDVAEAVIYVL 240
Qy	241 STPAHQIGDIQMRPTEQVT 260
Dd	241 STPAHQIGDIQMRPTEQVT 260

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RESULT 6
US-10-208-024-378
  Sequence 378, Application US/10208024
  Publication No. US20040048335A1
GENERAL INFORMATION:
  APPLICANT: Baker, Kevin P.
  APPLICANT: Chen, Jian
  APPLICANT: Desnoyers, Luc
  APPLICANT: Goddard, Audrey
  APPLICANT: Godowski, Paul J.
  APPLICANT: Gurney, Austin L.
  APPLICANT: Pan, James
  APPLICANT: Smith, Victoria
  APPLICANT: Watanabe, Colin K.
  APPLICANT: Wood, William I.
  APPLICANT: Zhang, Zenin
  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
  FILE REFERENCE: P2430R1C538
  CURRENT APPLICATION NUMBER: US/10/208,024
  CURRENT FILING DATE: 2002-07-29
  PRIOR APPLICATION NUMBER: 10/052586
  PRIOR FILING DATE: 2002-01-15
  PRIOR APPLICATION NUMBER: 60/059263
  PRIOR FILING DATE: 1997-09-18
  PRIOR APPLICATION NUMBER: 60/059266
  PRIOR FILING DATE: 1997-09-18
  PRIOR APPLICATION NUMBER: 60/062250
  PRIOR FILING DATE: 1997-10-17
  PRIOR APPLICATION NUMBER: 60/063120
  PRIOR FILING DATE: 1997-10-24
  PRIOR APPLICATION NUMBER: 60/063121
  PRIOR FILING DATE: 1997-10-24
  PRIOR APPLICATION NUMBER: 60/063486
  PRIOR FILING DATE: 1997-10-21
  PRIOR APPLICATION NUMBER: 60/063540
  PRIOR FILING DATE: 1997-10-28
  PRIOR APPLICATION NUMBER: 60/063541
  PRIOR FILING DATE: 1997-10-28
  PRIOR APPLICATION NUMBER: 60/063544
  PRIOR FILING DATE: 1997-10-28
  PRIOR Application data removed - See File Wrapper or PALM.
  NUMBER OF SEQ ID NOS: 612
  SEQ ID NO 378
  LENGTH: 260
  TYPE: PRT
  ORGANISM: Homo Sapien
US-10-208-024-378

```

	Query Match	100.0%	Score 1337	DB 12	Length 260
	Best Local Similarity	100.0%	Pred. No. 6.6e-132		
	Matches 260	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	MARPGMERWRDLRLVTGASGGIGAAVARALVQQGLKVVGCCARTVGNIEELAAECKSAGY	60		
Db	1	MARPGMERWRDLRLVTGASGGIGAAVARALVQQGLKVVGCCARTVGNIEELAAECKSAGY	60		
Qy	61	PGTLIPYRCDLSNEEDILSMFSAIRSOHSGVDI CINNAGLARPPTLTSGSTSGWKDMPNV	120		

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Db      61  PGTLPYRCDLSNEEDILSMFSAIRSOHSGVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120
QY      121  NVLALSICTREAYQSMKERNVDDGHIININSMGHRVLPVLSVTHFYFSATKYAVTALTGL 180
Db      121  NVLALSICTREAYQSMKERNVDDGHIININSMGHRVLPVLSVTHFYFSATKYAVTALTGL 180
QY      181  RQELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATVEQMKCLKPEDVAEAVIYVL 240
Db      181  RQELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATVEQMKCLKPEDVAEAVIYVL 240
QY      241  STPAHIIQIGDIQMRPTEQVT 260
Db      241  STPAHIIQIGDIQMRPTEQVT 260

RESULT 7
US-10-201-853-378
; Sequence 378, Application US/10201853
; Publication No. US20040053358A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C465
; CURRENT APPLICATION NUMBER: US/10/201,853
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 378
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-201-853-378

```

	Query Match	100.0%	Score 1337;	DB 12;	Length 260;
	Best Local Similarity	100.0%;	Pred. NO. 6.ee-132;		
	Matches 260;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MAREPGEWRDRRLALVTGASGGIGAAVARALVQGLKVGCARTVGNIIEELAECKSAGY	60		
Dd	1	MAREPGEWRDRRLALVTGASGGIGAAVARALVQGLKVGCARTVGNIIEELAECKSAGY	60		
Qy	61	PGTLIPYRCDLSNEEDILSMFSFAIRSQHSQGVDCINNAGLARPTLLSGSTSGWKMDFNV	120		

Db 61 PGTLPYRCDSLNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLLSGSTSGWKDMFNV 120
QY 121 NVLALSICTREAYQSMKERNVDDGHIININSMGSHRVLPLSVTHFYSAKYAVTALTTEGL 180
Db 121 NVLALSICTREAYQSMKERNVDDGHIININSMGSHRVLPLSVTHFYSAKYAVTALTTEGL 180
QY 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKLKPEDVAEAVIYVL 240
Db 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKLKPEDVAEAVIYVL 240
QY 241 STPAHIQIGDIQMRPTEQVT 260
Db 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 8

US-10-063-745-128
; Sequence 128, Application US/10063745
; Publication No. US20040058411A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,745
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 128
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-745-128

Query Match 100.0%; Score 1337; DB 12; Length 260;
Best Local Similarity 100.0%; Pred. No. 6.6e-132;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNTEELAAECKSAGY 60
Db 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNTEELAAECKSAGY 60
QY 61 PGTLPYRCDSLNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLLSGSTSGWKDMFNV 120
Db 61 PGTLPYRCDSLNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLLSGSTSGWKDMFNV 120
QY 121 NVLALSICTREAYQSMKERNVDDGHIININSMGSHRVLPLSVTHFYSAKYAVTALTTEGL 180
Db 121 NVLALSICTREAYQSMKERNVDDGHIININSMGSHRVLPLSVTHFYSAKYAVTALTTEGL 180
QY 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKLKPEDVAEAVIYVL 240
Db 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKLKPEDVAEAVIYVL 240
QY 241 STPAHIQIGDIQMRPTEQVT 260
Db 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 9

US-10-063-512-128
; Sequence 128, Application US/10063512
; Publication No. US20030018183A1
; GENERAL INFORMATION:

; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 128
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-512-128

Query Match 100.0%; Score 1337; DB 12; Length 260;
Best Local Similarity 100.0%; Pred. No. 6.6e-132;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNTEELAAECKSAGY 60
Db 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNTEELAAECKSAGY 60
QY 61 PGTLPYRCDSLNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLLSGSTSGWKDMFNV 120
Db 61 PGTLPYRCDSLNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLLSGSTSGWKDMFNV 120
QY 121 NVLALSICTREAYQSMKERNVDDGHIININSMGSHRVLPLSVTHFYSAKYAVTALTTEGL 180
Db 121 NVLALSICTREAYQSMKERNVDDGHIININSMGSHRVLPLSVTHFYSAKYAVTALTTEGL 180
QY 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKLKPEDVAEAVIYVL 240
Db 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKLKPEDVAEAVIYVL 240
QY 241 STPAHIQIGDIQMRPTEQVT 260
Db 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 10

US-10-063-513-128
; Sequence 128, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,513
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 128
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-513-128

Query Match 100.0%; Score 1337; DB 12; Length 260;
Best Local Similarity 100.0%; Pred. No. 6.6e-132;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNTEELAAECKSAGY 60
DB 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNTEELAAECKSAGY 60

QY 61 PGTLPYRCDLSNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120
DB 61 PGTLPYRCDLSNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120

QY 121 NVLALSICTRAYQSMKERNVDDGHIININSMGHRVPLSVTHFYFSATKYAVTALTEGL 180
DB 121 NVLALSICTRAYQSMKERNVDDGHIININSMGHRVPLSVTHFYFSATKYAVTALTEGL 180

QY 181 ROELREAQTHIRATCISPGVWETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
DB 181 ROELREAQTHIRATCISPGVWETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240

QY 241 STPAHIQIGDIQMRPTEQVT 260
DB 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 11
US-10-063-515-128
; Sequence 128, Application US/10063515
; Publication No. US20030018173A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,515
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 128
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-515-128

Query Match 100.0%; Score 1337; DB 12; Length 260;
Best Local Similarity 100.0%; Pred. No. 6.6e-132;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNTEELAAECKSAGY 60
DB 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNTEELAAECKSAGY 60

QY 61 PGTLPYRCDLSNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120
DB 61 PGTLPYRCDLSNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120

QY 121 NVLALSICTRAYQSMKERNVDDGHIININSMGHRVPLSVTHFYFSATKYAVTALTEGL 180
DB 121 NVLALSICTRAYQSMKERNVDDGHIININSMGHRVPLSVTHFYFSATKYAVTALTEGL 180

QY 181 ROELREAQTHIRATCISPGVWETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
DB 181 ROELREAQTHIRATCISPGVWETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240

QY 241 STPAHIQIGDIQMRPTEQVT 260
DB 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 12
US-10-063-549-128
; Sequence 128, Application US/10063549
; Publication No. US20030027986A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,549
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 128
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-549-128

Query Match 100.0%; Score 1337; DB 12; Length 260;
Best Local Similarity 100.0%; Pred. No. 6.6e-132;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNTEELAAECKSAGY 60
DB 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNTEELAAECKSAGY 60

QY 61 PGTLPYRCDLSNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120
DB 61 PGTLPYRCDLSNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120

QY 121 NVLALSICTRAYQSMKERNVDDGHIININSMGHRVPLSVTHFYFSATKYAVTALTEGL 180
DB 121 NVLALSICTRAYQSMKERNVDDGHIININSMGHRVPLSVTHFYFSATKYAVTALTEGL 180

QY 181 ROELREAQTHIRATCISPGVWETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
DB 181 ROELREAQTHIRATCISPGVWETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240

QY 241 STPAHIQIGDIQMRPTEQVT 260
DB 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 13
US-10-063-569-128
; Sequence 128, Application US/10063569
; Publication No. US20030018168A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,569
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 128
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-569-128


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; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,569
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 128
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-569-128

Query Match      100.0%; Score 1337; DB 12; Length 260;
Best Local Similarity 100.0%; Pred. No. 6.6e-132;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARFGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAITVGNTEELAAECKSAGY 60
Db 1 MARFGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAITVGNTEELAAECKSAGY 60
QY 61 PGTLPYRCDSLNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120
Db 61 PGTLPYRCDSLNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120
QY 121 NVLALSICTREAYOSMKERNVDDGHIININSMGSHRVLPLSVTHFYSAKYAVTALTGL 180
Db 121 NVLALSICTREAYOSMKERNVDDGHIININSMGSHRVLPLSVTHFYSAKYAVTALTGL 180
QY 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
Db 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
QY 241 STPAHIQIGDIQMRPTEQVT 260
Db 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 15
US-10-174-581-378
; Sequence 378, Application US/10174581
; Publication No. US20030017540A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C41
; CURRENT APPLICATION NUMBER: US/10/174,581
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063564
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063734
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063870
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066120
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066466
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069335

RESULT 14
US-10-063-551-128
; Sequence 128, Application US/10063551
; Publication No. US20020183494A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerriksen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,551
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 128
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-551-128

Query Match      100.0%; Score 1337; DB 12; Length 260;
Best Local Similarity 100.0%; Pred. No. 6.6e-132;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARFGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAITVGNTEELAAECKSAGY 60
Db 1 MARFGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAITVGNTEELAAECKSAGY 60
QY 61 PGTLPYRCDSLNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120
Db 61 PGTLPYRCDSLNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV 120
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Best Local Similarity 100.0%; Pred. No. 6.6e-132;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARPGMERWRDELALVTGASGGIGAAVARALVQQGLKVVGCAARTVGNIEELAAECKSAGY 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
QY 1 MARPGMERWRDELALVTGASGGIGAAVARALVQQGLKVVGCAARTVGNIEELAAECKSAGY 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 PGTLLPYRCDSLNEEDIILSMFSAIRSOHSGVDICINNAGLARPDPTLLSGSTSGWKDMENV 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 PGTLLPYRCDSLNEEDIILSMFSAIRSOHSGVDICINNAGLARPDPTLLSGSTSGWKDMENV 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 NVLALSICTREAYQSMKERNVDDGHIININSMGHRVLPVLSVTHFYSAVKYAVTALTEGL 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 NVLALSICTREAYQSMKERNVDDGHIININSMGHRVLPVLSVTHFYSAVKYAVTALTEGL 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 181 ROELREAOQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 181 ROELREAOQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 241 STPAHIQIGDIQMRPTEQVT 260
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 241 STPAHIQIGDIQMRPTEQVT 260
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Search completed: September 15, 2004, 11:30:57
Job time : 53 secs

Black

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: September 15, 2004, 11:20:22 ; Search time 40 Seconds
(without alignments)
625.245 Million cell updates/sec

Title: US-10-063-735-128
Perfect score: 1337
Sequence: 1 MARPQMERWRDLALVTGAS.....STPAHIQIGDIQMRPTEQVT 260

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	368	27.5	257	A81866	hypothetical prote
2	355.5	26.6	273	D81878	probable oxidoredu
3	353.5	26.4	273	H81140	oxidoreductase, sh
4	351	26.3	231	G30050	hypothetical prote
5	349.5	26.1	240	D95420	probable oxidoredu
6	348.5	26.1	255	T44991	oxidoreductase [im
7	334.5	25.0	244	AH2073	oxidoreductase air
8	332	24.8	249	E95283	probable [imported
9	331.5	24.8	240	A12681	oxidoreductase Atu
10	331.5	24.8	248	A10678	probable oxidoredu
11	331.5	24.6	271	G97463	probable oxidoredu
12	329.5	24.6	248	F64908	probable dehydroge
13	328.5	24.6	248	D90897	probable oxidoredu
14	328.5	24.6	248	C85720	probable oxidoredu
15	326.5	24.4	253	A95223	hypothetical prote
16	325.5	24.3	240	B99667	probable oxidoredu
17	325.5	24.3	240	F85517	probable oxidoredu
18	325.5	24.3	260	G84171	oxidoreductase [im
19	323.5	24.2	244	S76993	hypothetical prote
20	317.5	23.7	252	H64122	ydFG protein - Hae
21	315.5	23.6	253	C98087	oxidoreductase (EC
22	314.5	23.5	238	D69930	probable 3-oxoacyl
23	301.5	22.6	250	B71859	probable oxidoredu
24	299	22.4	239	G82383	oxidoreductase, sh
25	298	22.3	250	B86817	oxidoreductase ypi
26	296	22.1	231	JC7768	blue fluorescent p
27	295	22.1	251	D70743	hypothetical prote
28	293.5	22.0	250	E64564	short chain alchoh
29	293	21.9	267	S57593	hypothetical prote

30 290.5 21.7 260 2 T36118 probable oxidoredu
31 288 21.5 255 2 AF2466 hypothetical prote
32 278.5 20.8 249 2 JC7857 NADP+-dependent se
33 278 20.8 248 2 T44932 3-oxoacyl-[acyl-ca
34 278 20.8 259 2 A69965 ketoacyl reductase
35 276 20.6 255 2 D70635 hypothetical prote
36 275.5 20.6 249 2 AH3061 serine dehydrogena
37 275.5 20.6 249 2 G98224 serine dehydrogena
38 274.5 20.5 245 2 AG3436 short-chain dehydr
39 274.5 20.5 307 2 E70082 glucose 1-dehydrog
40 273 20.4 233 2 T35242 probable oxidoredu
41 271.5 20.3 246 2 A69621 3-oxoacyl-[acyl-ca
42 270 20.2 247 2 F92643 oxidoreductase xfl
43 270 20.2 259 2 AD3082 short-chain dehydr
44 270 20.2 259 2 D98204 probable short-cha
45 269 20.1 246 2 H72219 3-oxoacyl-[acyl ca

ALIGNMENTS

hypothetical protein all0475 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AB1866
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, N.; Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anal
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AB1866
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-257 <KUR>
A:Cross-references: GB:BA000019; PIDN:BAB72433.1; PID:gl7129820; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all0475
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 27.5%; Score 368; DB 2; Length 257;
Best Local Similarity 34.0%; Pred.No.3.le-24;
Matches 86; Conservative 53; Mismatches 104; Indels 10; Gaps 6;

Qy 10 RDRALVTGASGGIGAAVARALVQGLKVVGCARTVGNIEELAAEC-KSAGYPGTLIYR 68
Db 5 KNQVLITGASSGGIGNACARIFAGAGAKLILAAARLARLQQLADELNQDFGVEIHL--Q 62
Qy 69 CDLSNEEDILSMFSAIRSOHSQSGVDICINAGLARP-DTLISGTSQWKMENNVNVALSI 127
Db 63 LDVDRPVSVEIAIAPLPAWSAIDILINNAGLSRGLKHGDIQDWEEMIDTNVKGLEY 122
Qy 128 CTRAYOSMKERNVDDGHIININSMCHRVLPUSVTHFYSA TKYAVTALTEGLRQELREA 187
Db 123 LTRYVVPQWNRG--RGHVNLGSIAGHOTYPPG--NVYCGTKAAVKAISEGLKQDL--L 176
Qy 188 QTHFRATCISPGVVETQFAFKLHDKDPEKAAATQEQMKLPEDVAEAVLYVLSTPAHIQ 247
Db 177 GTPVRVTSVDPGWVETEFSEVRFHGDTERRAKVYQGVNPLTTPEDVADVIFFCATRSRPHVN 236
Qy 248 IGDQMRPTEQVT 260
Db 237 INEVILMPVDAQS 249

RESULT 2
D81878
probable oxidoreductase NMA1120 [imported] - Neisseria meningitidis (strain 23491 serogr
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001

D95420
Probable oxidoreductase SM2343 [imported] - Sinorhizobium meliloti (strain 102)
C:Species: Sinorhizobium meliloti
C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
C:Accession: D95420
R:Barnett, M.J.; Fisher, R.P.; Jones, T.; Komp, C.; Abola, A.P.; Barlow-Hubler,
E.; Kalmann, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.;
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A:Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium


```

RESULT 11
G97463
probable oxidoreductase (AE005204) [imported] - Agrobacterium tumefaciens (strain C58, C
C:Species: Agrobacterium tumefaciens
C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C:Accession: G97463
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: G97463
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-271 <KUR>
A:Cross-references: GB:AE007869; PIDN:AAK86664.1; PID:g15155846; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C_1567
A:Map position: circular chromosome
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match      24.8%; Score 331.5; DB 2; Length 271;
Best Local Similarity 32.5%; Pred. No. 4.7e-21;
Matches      80; Conservative 47; Mismatches 108; Indels 11; Gaps 5;

QY 11 DRLALVTGASGGIGAAVARALVQOGLKVGCARTVGNIEELAAECKSAGYPTGLIPYRCD 70
Db 35 NKVVLTIGASSGIGGIAARELAGAKLVLGARRMDRLQSLABELRRKG--AEVVIHTLD 92

QY 71 LSNEEDILSMFSAIRSQHSQVDICINNAGLARPDTLTLLSGSTSGWKDMFNVNVALSICTR 130
Db 93 VTRQSVFAEAGKALGQIDIVNNAGIMPLSLMSLSLKVDWDRMLEVWKGLVYGYA 152

QY 131 EAYOSMKERNVDDGHIININSMGHRVPLSLSVTHFYSAKYAVTALTTEGLRQELREAQTH 190
Db 153 AVLPEMTAR--ASGHIINIASIGALAVSPTRA--YCATKFAVRAISDGLQENRD---- 204

QY 191 IRATCISPGVVEQAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIVLSTPAAHIQIGD 250
Db 205 LRVTCHIFGVVESELAHTITDPAAELMQSYRAI--ALKPDAIGRAVRYAIEQPDVDVNE 263

QY 251 IQMRPT 256
Db 264 IVIRPT 269

RESULT 12
F64908
probable dehydrogenase (EC 1.1.1.1-) ydFG - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: F64908
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: F64908
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-248 <BIAT>
A:Cross-references: GB:AE000251; GB:U00096; MID:g1787814; PIDN:AACT4612.1; PID:g1787820;
A:Experimental source: strain K-12, substrain MGI655
C:Genetics:
A:Gene: ydFG
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C:Keywords: oxidoreductase
F:1-178/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match      24.6%; Score 329.5; DB 2; Length 248;
Best Local Similarity 35.9%; Pred. No. 6.2e-21;
Matches      89; Conservative 34; Mismatches 112; Indels 13; Gaps 6;

QY 13 LALVTGASGGIGAAVARALVQOGLKVGCARTVGNIEELAAECKSAGYPTGLIPYRCDLS 72
Db 2 IVLVGTAGAGFECITRRFIQQGHKVIATGRQRERLQELKDELGNLYIAQL-----DVR 56

QY 73 NEEDILSMFSAIRSQHSQVDICINNAGLA-RPDTLLSGSTSGWKDMFNVNVALSICTRE 131
Db 57 NRAAIEEMLASLPAEWCNIDILVNNAGLALGMEPAHKASIEDMETMTNNKGLVYMTRA 116

QY 132 AYOSMKERNVDDGHIININSMGHRVPLSLSVTHFYSAKYAVTALTTEGLRQELREAQTH 191
Db 117 VLPGMVERN--HGHIINIGSTAGS--WYAGGNVYGATKAFVRQFSLNRLTDLH--GTAV 170

QY 192 RATCISPGVV-ETQAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIVLSTPAAHIQIGD 250
Db 171 RVTDIIEPLGVGTEFSNVRFGDGGKAEKTYQNTVALTPEDVSEAVVWVSTLPAHVNT 230

QY 251 IQMRPT 258
Db 231 LEMMPVTQ 238

RESULT 13
D90897
probable oxidoreductase ECs2148 [imported] - Escherichia coli (strain O157:H7, substrain
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: D90897
R:Havashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: D90897
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-248 <HAY>
A:Cross-references: GB:BA000007; PIDN:BA835571.1; PID:g13361614; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs2148
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match      24.6%; Score 328.5; DB 2; Length 248;
Best Local Similarity 35.9%; Pred. No. 7.6e-21;
Matches      89; Conservative 34; Mismatches 112; Indels 13; Gaps 6;

QY 13 LALVTGASGGIGAAVARALVQOGLKVGCARTVGNIEELAAECKSAGYPTGLIPYRCDLS 72
Db 2 IVLVGTAGAGFECITRRFIQQGHKVIATGRQRERLQELKDELGNLYIAQL-----DVR 56

QY 73 NEEDILSMFSAIRSQHSQVDICINNAGLA-RPDTLLSGSTSGWKDMFNVNVALSICTRE 131
Db 57 NRAAIEEMLASLPAEWCNIDILVNNAGLALGMEPAHKASIEDMETMTNNKGLVYMTRA 116

QY 132 AYOSMKERNVDDGHIININSMGHRVPLSLSVTHFYSAKYAVTALTTEGLRQELREAQTH 191
Db 117 VLPGMVERN--HGHIINIGSTAGS--WYAGGNVYGATKAFVRQFSLNRLTDLH--GTAV 170

QY 192 RATCISPGVV-ETQAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIVLSTPAAHIQIGD 250
Db 171 RVTDIIEPLGVGTEFSNVRFGDGGKAEKTYQNTVALTPEDVSEAVVWVSTLPAHVNT 230

QY 251 IQMRPT 258
Db 231 LEMMPVTQ 238

RESULT 14
C85720
probable oxidoreductase ydFG [imported] - Escherichia coli (strain O157:H7, substrain EDI
C:Species: Escherichia coli

```

C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C/Accession: C85720
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A>Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: C85720
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-248 <STO>
A/Cross-references: GB:AE005174; MID:g12515117; PIDN:AA656223.1; GSPDB:GN00145; UWGP:2001
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Gene: ydfg
C/Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 24.4%; Score 326.5; DB 2; Length 248;
Best Local Similarity 35.9%; Pred. No. 7.6e-21;
Matches 89; Conservative 34; Mismatches 112; Indels 13; Gaps 6;

Qy 13 LALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNIEELAAECKSAGYPGTLIPYRCDLS 72
Db 2 IVLVTGATAGGECITRRFIOQGHKVIATGRRQERLQDELGDNLVIAQL-----DVR 56
Qy 73 NEEDILSMFSAIRSOHSGVDICINNAGLA-RPDTLLSGSTSGWKDMFNVNVALISICTRE 131
Db 57 NRAAIEMLASLPAWCNIDILVNAGLALGMPEAHKASIEDWETMTIDTNKGLVYVTRA 116
Qy 132 AYQSMKERNVDDGHIININSGSHRVLPLSVTHFYSAKYAVTALTEGLRQELREAQTHI 191
Db 117 VLPQWVRN--HGHIINIGTAGS--WPYAGNVYGATKAFVRQFSNLNRDILH--GTAV 170
Qy 192 RATCISPGWV-ETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVYVLSTFAHIQIGD 250
Db 171 RVTDIEFLGVGTFFSVRFKGDGKAEKTYQNTVALTPTEDVSEAVWVSTLPAHVNI 230
Qy 251 IQMPPTQ 258
Db 231 LEMMPVTQ 238

RESULT 15
A95223
hypothetical protein SPI909 [imported] - Streptococcus pneumoniae (strain TIGR4)
C/Species: Streptococcus pneumoniae
C/Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C/Accession: A95223
R/Tetelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Unayam, L.A.; White, C.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzap
son, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A/Authors: Lofcus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A/Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.
A/Reference number: A95000; MUID:21357209; PMID:11463916
A/Accession: A95223
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-253 <CUR>
A/Cross-references: GB:AE005672; PIDN:AAK75978.1; PID:g14973413; GSPDB:GN00164; TIGR:SPA
A/Experimental source: strain TIGR4
C/Genetics:
A/Gene: SPI909
C/Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 24.4%; Score 326.5; DB 2; Length 253;
Best Local Similarity 33.5%; Pred. No. 1.2e-20;
Matches 85; Conservative 48; Mismatches 100; Indels 21; Gaps 5;

Qy 15 LVTGASGGIGAAVARALVQOGLKVVGCAARTVGNIEELAAECKSAGYPGTLIPYRCDLSNE 74
Db 6 VITGATSGIGAIARVLEQGEDVLTGRRIDRLKAEFAETFPNQVTWTFLLDVTDM 65

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2004, 11:24:07 ; Search time 32 Seconds
(without alignments)
419.461 Million cell updates/sec

Title: US-10-063-735-128
Perfect score: 1337
Sequence: 1 MARPCMERWRDLALVTGAS.....STPAHIQIGDIQMRPTEQVT 260

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/2/iaa/5B COMB.pbp:*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pbp:*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pbp:*
5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pbp:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pbp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	337.5	25.2	249	4	US-09-543-681A-4882
2	331	24.8	249	4	US-09-134-000C-5219
3	317	23.7	265	4	US-09-328-352-6325
4	316.5	23.7	231	4	US-09-134-001C-4397
5	308.5	23.1	272	4	US-09-489-039A-13748
6	308	23.0	248	3	US-09-385-028-11
7	308	23.0	248	4	US-09-726-614-11
8	308	23.0	248	4	US-09-385-040-11
9	307	23.0	256	4	US-09-107-532A-4541
10	269	20.1	288	4	US-09-328-352-6485
11	262.5	19.6	262	4	US-09-328-352-4761
12	232.5	18.9	632	4	US-09-252-991A-23096
13	252	18.8	262	4	US-09-134-000C-4224
14	252	18.8	294	4	US-09-328-352-4992
15	251.5	18.8	256	4	US-09-252-991A-30474
16	250	18.7	742	4	US-09-252-991A-24489
17	249	18.6	266	4	US-09-489-039A-12759
18	247.5	18.5	315	3	US-08-793-035-9
19	247.5	18.5	315	3	US-08-793-035-10
20	239.5	17.9	333	1	US-08-440-856A-4
21	239	17.9	278	4	US-09-489-039A-7309
22	239	17.9	300	4	US-09-976-594-7
23	237.5	17.8	301	4	US-09-252-991A-24032
24	237.5	17.8	337	1	US-08-440-856A-3
25	236.5	17.7	244	1	US-08-762-129-4
26	234.5	17.5	244	1	US-08-762-129-3
27	233.5	17.5	300	4	US-09-907-794A-159

28	233.5	17.5	300	4	US-09-866-028-37	Sequence 37, Appl
29	233.5	17.5	300	4	US-09-905-125A-159	Sequence 159, App
30	233.5	17.5	300	4	US-09-902-775A-159	Sequence 159, App
31	233.5	17.5	301	4	US-09-288-143-98	Sequence 98, Appl
32	232.5	17.4	292	4	US-09-489-039A-12880	Sequence 12880, A
33	232	17.4	246	4	US-08-178-257-9	Sequence 9, Appli
34	232	17.4	279	4	US-09-540-236-3794	Sequence 3794, Ap
35	231	17.3	265	4	US-09-543-681A-7082	Sequence 7082, Ap
36	230.5	17.2	244	2	US-09-090-567-2	Sequence 2, Appli
37	227.5	17.0	246	3	US-09-238-481-2	Sequence 2, Appli
38	227.5	17.0	246	4	US-09-572-810A-2	Sequence 2, Appli
39	226.5	16.9	262	4	US-09-489-039A-11983	Sequence 11983, A
40	225	16.8	254	4	US-09-543-681A-7648	Sequence 7648, Ap
41	224	16.8	250	4	US-09-489-039A-9604	Sequence 9604, Ap
42	223	16.7	203	4	US-09-634-955B-20	Sequence 20, Appl
43	223	16.7	203	4	US-09-634-955B-26	Sequence 26, Appl
44	222.5	16.6	259	4	US-09-252-991A-28945	Sequence 28945, A
45	221.5	16.6	246	4	US-08-178-257-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
US-09-543-681A-4882
; Sequence 4882, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543.681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4882
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-4882

Query Match	25.2%	Score	337.5	DB 4	Length	249			
Best Local Similarity	35.2%	Pred. No.	1.1e-29						
Matches	88	Conservative	39	Mismatches	106	Indels	17	Gaps	7
QY	13	LALVTGASGGIGAAVARALVQOGLKVVGCARTVGNIEELAAECKSAGYPTGLIPYRCDLS	72						
Db	2	IIFITGASAGFGEAIAHFHINHGKVI GTARRLDKQLQALHQLGDLFY-----PLQLDVT	56						
QY	73	NEEDILNMFSAIRSQHSQGVDCINNAGLA---RPDTLLSGSTSGWKDMENVNVLALSICT	129						
Db	57	DKKAVSEIYHQLPEQWRSDVLINNAGLGLRP--VDKANLDDWDITMETNKGVLHVHT	114						
QY	130	REAYQSKMERVDDGHIININSMGHRVLPUSVTHFSATKYAVTALTEGRLQELREAO	189						
Db	115	RALLPSMVERN--GHINISSTAAS--WPTMGNNVYGATKAFVKQFSLGRADLQGGK-	169						
QY	190	HIRATCISPGVV-ETQFAFKLHDKDPEKAAATYBQMKLCPEDVAEAYIVYLSTPAHTOI	248						
Db	170	IRVTDIEPLVGUGTEFSLVRFKGDITKVEQTYACADALTPEDVAQVFWTATLPAHVNI	228						
QY	249	GDIQMRPTEQ	258						
Db	229	NTELEMPVSO	238						

RESULT 2
US-09-134-000C-5219
; Sequence 5219, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:

```

; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5219
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5219

Query Match      24.8%; Score 331; DB 4; Length 249;
Best Local Similarity 31.9%; Pred.No.6,1e-29;
Matches      82; Conservative 54; Mismatches 103; Indels 18; Gaps 7

Qy      6 MERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAETVGNIBELAAECKSAGYPGTLI 65
      | : : : | | | | | : : : | : : : | : : : | : : : | : : : | : : :
Db      5 MKSLSEKVVIMGASSGIGETARLLARKGAKLVIAARRQERLIAIKKELPEA---TIL 60

Qy      66 PYRCDLSENEEDILSFWFSAIRQSHSGVDICINNAGLARPDITLLSGSTSGWKMFNVNVAL 125
      | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db      61 VQQADVTKEEVSQVRVIKLTMEKYGIDVLFNNAGVMPAPTLEAPKGEWRQMLDINIMGV 120

Qy      126 SICTREAVQSKERNVDDGHIININSMGHRVLPISVTHFYSATKYAVTALTEGLRQELR 185
      | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db      121 LNGIAAVLPIMVEOK--SGQIIATDSVAGHVVPYPSAV--YCGTFAFAVRAIMEGRQQR 176

Qy      186 EAQTHIRATCISPGVETQFAFKLHDKDPEKAAAT---YEQMKC-LKPEDVAEAEIYVILS 241
      | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :
Db      177 E--NNIKSTIISPGAVQTE-----LYQTISNRVVAETLHLEQLSWGLKAEIDTAQAVVPAID 230

Qy      242 TPAHIQIGDIQMRPTEQ 258
Db      231 TPDRMSISEMVRPTQ 247

```

```

RESULT 3
US-09-328-352-6325
; Sequence 6325, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6325
; LENGTH: 265
; TYPE: FRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6325

```

Query Match	23.7%	Score 317;	DB 4;	Length 265;
Best Local Similarity	34.7%	Pred. No. 2.5e-27;		
Matches	87;	Conservative 41;	Mismatches 107;	Indels 16; Gaps 8;

Qy	13	LALVTGASGGTGA	AVARALVOOGLKWGCARTVGNIEELAAECKSAGYPGTLIPYRCDLS	72
Db	15	LALVTGASAGFYSISKLI	ESGYKVICGRRAEKLEELQKLGENFYPLVF----	DMT 69
Qy	73	N-EDILSMFSAIRS--	QHSGVDICINNAGLARP-DTLLSGSTSGWKDMFNVLALSGIC	128
Db	70	DTAENINKLFXELPNE	FOIDQLLVNAGLALGLEPADKADLDWYTMIDTNVKGVLTV	129
Qy	129	TREAYQMKERNVDGHI	ININSMGSHRVLPPLSVTHFYFSATKYAVTALTGELRQELREAQ	188

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Db      130  TRILPSMVKK--SGLIIMGSTAG--TYPYPGNVYGATKAFVEQFSLNRLADI--AG 183
Qy      189  THIRATCISPGW-ETQFAFKLHKDPEKAAATYEQMKCLXPEDVAEAVIYVLSTPAHIQ 247
Db      184  TGVRTVNIPEGLCGGTFSLVRFKGDQEKANSLSYDKKNPILPEDIANTVAMIASOPPHIN 243
Qy      248  IGDIQMRPTEQ 258
Db      244  INRIEMPTTQ 254

RESULT 4
US-09-134-001C-4397
; Sequence 4397, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: LYTH Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHY-
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134.001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4397
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4397

```

Query Match	23.7%	Score	316.5	DB	4	Length	231
Best local Similarity	29.9%	Pred. No.	2.3e-27				
Matches	75	Conservative	56	Mismatches	97	Indels	23
Gaps							
Qy	6	MERWRDLALVTGASGCGIGAAVARALVQOGLKVVGCA	RTVGNIBELAAECKSAGYPGTLI	65			
		: : : : : :	: : : : : :				
Db	2	MAKVKEKVVAVVTGASSGIGEAIAKLSQOQASIVLVGR	NEQLNNEIVQQLNN--PAKVV	58			
		: : : : : :	: : : : : :				
Qy	66	PYRCDSLSEEDILMSFAIRBSQHSQVDCINNAGLARP	DTLLSGTSGWKDMFNVL-A	124			
		: : : : : :	: : : : : :				
Db	59	--TADVTVKNSIDMLKAVIDHFGHIDI VNSAGQSLSS	KITDYNVEQWDTMIDVNIKGT	116			
		: : : : : :	: : : : : :				
Qy	125	LSICTREAYQSMKERNVDGHHININSMSGHRVLP	SVTHFYFSAKVAVTALTEGLRQEL	184			
		: : : : : :	: : : : : :				
Db	117	LHVLAQATLPYLLKQ--SSGHIINLASVSGFE--P	TKTNVAVYGATKAAIHAITQSLEKEL	171			
		: : : : : :	: : : : : :				
Qy	185	REAQTHIRATCISPGVVETQFAFKLHDQDEKAAAT	YEQMKCLPQEDVAEAVIYVLTSPA	244			
		: : : : : :	: : : : : :				
Db	172	--ARTGVKVTISI PGWVDT-----PMTEGTFGER	KKLEQAQNIADAVVYLTQPS	219			
		: : : : : :	: : : : : :				
Qy	245	HIQIGDIQMRP	255				
		: : : : : :	: : : : : :				
Db	220	HVNNVNEVTRP	230				
		: : : : : :	: : : : : :				

RESULT 5
US-09-489-039A-13748
; Sequence 13748, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13748

[illegible]

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-726-614-11

Query Match      23.0%; Score 308; DB 4; Length 248;
Best Local Similarity 31.3%; Pred. No. 2.4e-26;
Matches 78; Conservative 50; Mismatches 111; Indels 10; Gaps 5;

QY 12 RLALVTGASGGIGAAVARALVQOGLKVVGCARTVGNIEELAAECKSAGYPTGLIPYRCDL 71
DB 8 KVALITGASSGIGETARALAAEAGAAVAIAARRVEKRLAGDELTAAGAKVHVL--ELDV 65

QY 72 SNEEDILSMFSAIRSOHSGVDICINNAGLAPDPTLLSGSTSGWKDMFNVNVLALSICTRE 131
DB 66 ADRQGVDAAVATVEALGGLDILVNNAGIMLGPVEDADTTDMTRMIDNLLGLMYMTRA 125

QY 132 AYQSMKERNVDDGHIININSMGHRVPLSVTHFYSAKYAVTALTEGLRQELREAQTHI 191
DB 126 ALPHILR---SKGTVVQSSIAGR--VNVRNAAVQATKFGVNAFSETLRQEVTE--RGV 178

QY 192 RATCISPGVETQFAFKL-HDKDPEKAAATYEQMKCLKPEDVAEAVIYVLTSTPAHIQIGD 250
DB 179 RVVVIPTGTTDLRGHITHTATKEMYEORISQIRKLOAQDIAEAVRYAVTAPHATVHE 238

QY 251 IQMRPTQV 259
DB 239 IFIRPTQV 247

RESULT 8
US-09-385-040-11
; Sequence 11, Application US/09385040
; Patent No. 6589775
; GENERAL INFORMATION:
; APPLICANT: Jensen, Susan E
; APPLICANT: Aidoo, Kwamena A
; APPLICANT: Parakkar, Ashish S
; TITLE OF INVENTION: DNA SEQUENCE ENCODING ENZYMES OF CLAVULANIC ACID
; TITLE OF INVENTION: BIOSYNTHESIS
; FILE REFERENCE: 09/385,040
; CURRENT APPLICATION NUMBER: US/09/385,040
; CURRENT FILING DATE: 1999-08-30
; PRIOR APPLICATION NUMBER: US 08/790,462
; PRIOR FILING DATE: 1997-01-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Streptomyces clavuligerus
US-09-385-040-11

Query Match      23.0%; Score 308; DB 4; Length 248;
Best Local Similarity 31.3%; Pred. No. 2.4e-26;
Matches 78; Conservative 50; Mismatches 111; Indels 10; Gaps 5;

QY 12 RLALVTGASGGIGAAVARALVQOGLKVVGCARTVGNIEELAAECKSAGYPTGLIPYRCDL 71
DB 8 KVALITGASSGIGETARALAAEAGAAVAIAARRVEKRLAGDELTAAGAKVHVL--ELDV 65

QY 72 SNEEDILSMFSAIRSOHSGVDICINNAGLAPDPTLLSGSTSGWKDMFNVNVLALSICTRE 131
DB 66 ADRQGVDAAVATVEALGGLDILVNNAGIMLGPVEDADTTDMTRMIDNLLGLMYMTRA 125

QY 132 AYQSMKERNVDDGHIININSMGHRVPLSVTHFYSAKYAVTALTEGLRQELREAQTHI 191
DB 126 ALPHILR---SKGTVVQSSIAGR--VNVRNAAVQATKFGVNAFSETLRQEVTE--RGV 178

QY 192 RATCISPGVETQFAFKL-HDKDPEKAAATYEQMKCLKPEDVAEAVIYVLTSTPAHIQIGD 250
DB 179 RVVVIPTGTTDLRGHITHTATKEMYEORISQIRKLOAQDIAEAVRYAVTAPHATVHE 238

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-726-614-11

Query Match      23.0%; Score 307; DB 4; Length 256;
Best Local Similarity 30.4%; Pred. No. 3.2e-26;
Matches 76; Conservative 54; Mismatches 106; Indels 14; Gaps 6;

QY 11 DLRLAVTGASGGIGAAVARALVQOGLKVVGCARTVGNIEELAAECKSAGYPTGLIPYRCD 70
DB 17 EKVVIVMGASSGIGETATKLLAEKGAKLVIARREDRLKAIKESLPEA---ELYQTAD 72

QY 71 LNEEDILSMFSAIRSOHSGVDICINNAGLAPDPTLLSGSTSGWKDMFNVNVLALSICTR 130
DB 73 VRDFAQVQAVIDLAMEKFGRIIDVLYNNAGIMPTAPLVEGHRDEWQNMLDINIMGVNLS 132

QY 131 EAYQSMKERNVDDGHIININSMGHRVPLSVTHFYSAKYAVTALTEGLRQELREAQTH 190
DB 133 AVLPIMEKQK--SGHLLSTDSVAGHVYVDSAV--YCGTKFAVRAIMEGLRQQR--QNN 186

QY 191 IRATCISPGVETQFAFKLHDKDPEKAAATYEQMK--CLKPEDVAEAVIYVLTSTPAHIQ 248
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Db 187 IKSIISGAVQTELYQTISK--KAALHLEHAQKEWGLTSEDIASAVAFAIETPDRMSV 244
Qy 249 GDIQWRPTEQ 258
Db 245 SNMIIRPTQ 254

RESULT 10

US-09-328-352-6485
; Sequence 6485, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6485
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6485

Query Match 20.1%; Score 269; DB 4; Length 288;
Best Local Similarity 29.6%; Pred. No. 7.6e-22;
Matches 73; Conservative 50; Mismatches 96; Indels 28; Gaps 7;

Qy 6 MERWRDLALVTGASGGIGAARALVOOG-----LKVVGCAARTVGNIEELAECKSA 58
Db 5 MKSFKNVAAVTGAGSGIGQALALAKQCHLALSDISEAGLAKTV-----ELLAP---- 56
Qy 59 GYPOTLIPYRCDLSNEEDILSMFSAIRSOHSGVDICINNAGLARPDTLLSGSTSGWKDMF 118
Db 57 -YSKVTTQKVDVAKROEVATWAKAVVDEHGQVNLIFNNAGVAIGSTAEGVSYEDLEWLI 115
Qy 119 NVNVLALSICTREAYQSKERNVDDGHIININSMGHRVLPPLSVTHFYSAKYAVTALTE 178
Db 116 GINFWGVYGTKEFLPYLKQSG--DGHIIINISSMFLGTAQPTQSA--YNASKFAVRGFT 171
Qy 179 GLRQELREAQTHIRATCISPGVWETQF--AFKLHDK-----DPEKAAATYEQMKCLKPE 230
Db 172 SLRQELDMQNAVGTATVHPGIGIRNTIAKARMNSVQSLGMDPLKSDQADFKLIRPAD 231
Qy 231 DVAEAVI 237
Db 232 DAAQQIL 238

RESULT 11

US-09-328-352-4761
; Sequence 4761, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4761
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4761

Query Match 19.6%; Score 262.5; DB 4; Length 262;
Best Local Similarity 30.0%; Pred. No. 3.6e-21;
Matches 72; Conservative 49; Mismatches 108; Indels 11; Gaps 5;

Qy 12 RLALVTGASGGIGAARALVOOGLKVVGCARTVGNIEELAECKSAGYPGTLIPYRCDL 71
Db 24 KVALVTGASRGIGAIAAQLIQDGYFVVGTATSESGAOKLT--DSFGEQAGL--ALDV 78
Qy 72 SNEEDILSMFSAIRSOHSGVDICINNAGLARPDTLLSGSTSGWKDMFNVNVLALSICTRE 131
Db 79 RNLDEIEAVVSHIQNYGPFVLVYNNAGITKDNLLRMSEDDDDILNIHLKAVYRLSKR 138
Qy 132 AYQSKERNVDDGHIININSMGHRVLPPLSVTHFYSAKYAVTALTEGLRQELREAQTHI 191
Db 139 VLKGMTKARF--GRIINISSVVAHFANPGQAN--YSAKAGIEAFSRSLAKEMGSRQ--I 192
Qy 192 RATCISPGVWETQFAPKLHDKDPEKAAATYEQMKCLKPEDEVAEAVIYVLSLTPAHLIQIDI 251
Db 193 TVNSVAPGFIATMTDALSDIRKMSDQVALNGLGEFQDIANAVSFLASDKAGYITGTV 252

RESULT 12
US-09-252-991A-23096
; Sequence 23096, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23096
; LENGTH: 632
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23096

Query Match 18.9%; Score 252.5; DB 4; Length 632;
Best Local Similarity 27.4%; Pred. No. 2e-19;
Matches 74; Conservative 56; Mismatches 109; Indels 31; Gaps 9;

Qy 6 MERWRDLALVTGASGGIGAARALVOOGLKVVGCARTVGNIEELAECKSAGY-PGTL 64
Db 342 MKSFENKVAITGAGSGIGRALAVELGRQCHLADVNAAALBETRQLASSGVRVSTA 401
Qy 65 IPYRCDLSNEEDILSMFSAIRSOHSGVDICINNAGLARPDTLLSGSTSGWKDMFNVNVL 124
Db 402 V---VDVADREQVQAWADKAASEHGRVNLIFNNAGVAHAGTVEGSDYSEYEWNNINFWG 458
Qy 125 LSICTREAYQSKERNVDDGHIININSMGHRVLP-LSVTHFYSAKYAVTALTGLRQE 183
Db 459 VNGTKAFLPHLKASG--NGHVNVSVSVFGLFAQPGMSA---YNATKYAVRGFTESLRQE 513
Qy 184 LREAQTHIRATCISPGVWETQFA-----FKLHDKDPEKAAATY-EQMKCLKPEDEV 233
Db 514 LDMEDSGVSASCVHPGGIKNTIARTARMESMAKVGTGQAPDKAREQNDOLLRTTPEKAA 573
Qy 234 EAVI-----YVLSTPAHIQIDGIQMR 254
Db 574 QVILRGVQRDSRRLITGTDAHAI--DVMLR 601

RESULT 13

US-09-134-000C-4224
; Sequence 4224, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032

Search completed: September 15, 2004, 11:30:00
Job time : 33 secs

Query Match	18.8%;	Score 252;	DB 4;	Length 294;
Best Local Similarity	28.4%;	Pred. No. 6.6e-20;		
Matches	75;	Conservative 47;	Mismatches 10;	Indels 36; Gaps 9
QY	6	MERNRDLALVTGASGGIGAARVALVOOGLKVVGCARTVGNIBLAAECKSAGYPGT--	63	
DB	18	MKNFNKVAITGAGSGIGQQLAILLAQ-----GCHLSLDINE-----KGLQQTVE	65	
QY	64	-LIPY-----RCDLSNEEDIILSMFSAIRSQHSVGVDICINNAGLARPTDLLSGTSGW	114	
DB	66	LLKPYSNITVTTKLVDSDREAVKQWCAQETQDGHGSVNLIFNNAGVALGSTVEGATYEDL	125	
QY	115	KDMFNVAVALSICITREAYQSKERNVDVDDGHIININSMGSHRVLPSTVTHYFSATKYAVT	174	
DB	126	EWIVGINFWGVYGTKEFLPIKQ--TQDGHIIINISLFLGTAQP--TQSGYNATKFAVR	181	
QY	175	ALTEGLAQELREAOTHIRATCISPGVWTFQ--AFKLHDK-----DPEKAAATYEQMKC	226	
DB	182	GFTESLLQELDIKSGVSSLVHPGGIRNTAKAAKMSDSSLGLGMDPAKSIQNFDFKLR	241	
QY	227	LKPEDVAEAVI--YVLSTPAHIQIG	249	

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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 16, 2004, 16:23:41 : Search time 85 Seconds
(without alignments)
1697.497 Million cell updates/sec

Title: US-10-063-735-128

Perfect score: 1337

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 692709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

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Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
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-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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4: /cgn2_6/ptodata/2/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/2/ina/6CTUS.COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	337.5	25.2	750	4	US-09-543-681A-710
3	331	24.8	750	4	US-09-134-000C-1814
C 4	326.5	24.4	3149	4	US-08-961-527-31
5	326.5	24.4	6133	4	US-09-453-702B-15
6	322.5	24.1	1830121	4	US-09-557-884-1
7	322.5	24.1	1830121	4	US-09-643-980A-1
8	318	23.8	763	4	US-09-221-017B-723
9	317	23.7	798	4	US-09-328-352-2199
10	316.5	23.7	696	4	US-09-134-001C-1560
11	308.5	23.1	819	4	US-09-489-039A-6577
C 12	308	23.0	744	3	US-09-385-028-22

C 13	308	23.0	744	4	US-09-726-614-22	Sequence 22, Appl
C 14	308	23.0	744	4	US-09-385-040-22	Sequence 22, Appl
C 15	308	23.0	11604	3	US-09-385-028-13	Sequence 13, Appl
C 16	308	23.0	11604	4	US-09-726-614-13	Sequence 13, Appl
C 17	308	23.0	11604	4	US-09-385-040-13	Sequence 13, Appl
C 18	308	23.0	15079	3	US-09-385-028-1	Sequence 1, Appl
C 19	308	23.0	15079	4	US-09-726-614-1	Sequence 1, Appl
C 20	308	23.0	15120	4	US-09-385-040-1	Sequence 1, Appl
C 21	307	23.0	771	4	US-09-107-532A-887	Sequence 887, App
C 22	295	22.1	4403765	3	US-09-103-840A-2	Sequence 2, Appl
C 23	295	22.1	441529	3	US-09-103-840A-1	Sequence 1, Appl
C 24	269	20.1	867	4	US-09-328-352-2359	Sequence 2359, Ap
C 25	262.5	19.6	789	4	US-09-328-352-635	Sequence 635, App
C 26	252.5	18.9	1038	4	US-09-252-991A-6549	Sequence 6549, Ap
C 27	252.5	18.9	1899	4	US-09-252-991A-6525	Sequence 6525, Ap
C 28	252	18.8	789	4	US-09-134-000C-819	Sequence 819, App
C 29	252	18.8	885	4	US-09-328-352-866	Sequence 866, App
C 30	251.5	18.8	771	4	US-09-252-991A-13903	Sequence 13903, A
C 31	251.5	18.8	1995	4	US-09-252-991A-13546	Sequence 13546, A
C 32	250.5	18.7	6977	4	US-08-178-237-8	Sequence 8, Appl
C 33	250	18.7	996	4	US-09-252-991A-7849	Sequence 7849, Ap
C 34	250	18.7	1743	4	US-09-252-991A-7635	Sequence 7635, Ap
C 35	250	18.7	2229	4	US-09-252-991A-7918	Sequence 7918, Ap
C 36	249	18.6	801	4	US-09-489-039A-5588	Sequence 5588, Ap
C 37	249	18.6	31940	4	US-09-596-002-13	Sequence 13, Appl
C 38	247.5	18.5	1155	3	US-08-793-035-1	Sequence 2, Appl
C 39	247.5	18.5	1185	3	US-08-793-035-1	Sequence 1, Appl
C 40	247.5	18.5	1419	4	US-09-252-991A-13796	Sequence 13796, A
C 41	244.5	18.3	4403765	3	US-09-103-840A-2	Sequence 2, Appl
C 42	244.5	18.3	441529	3	US-09-103-840A-1	Sequence 1, Appl
C 43	239.5	17.9	1187	1	US-08-440-856A-2	Sequence 2, Appl
C 44	239	17.9	837	4	US-09-489-039A-138	Sequence 138, App
C 45	239	17.9	1010	4	US-09-976-594-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1

US-08-956-171E-330/c
; Sequence 330, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman


```

Query Match:      24.42%      Indels:      21
DB:               4          Gaps:        5

US-10-063-735-128 (1-260) x US-08-961-527-31 (1-3149)

QY 15 LeuValThrGlyAlaSerGlyGlyLeuGlyAlaAlaValAlaAlaValGlnGln 34
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1331 GTGATTACAGAGCGACATCAGGATCGTGAAGCATTTGGCGGTCTTCTGGAGCAG 1272

QY 35 GlyLeuYsValValGlyCysAlaAlaArgThrValGlyAsnIleGluGluLeuAlaGlu 54
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1271 GGTGAGGATGCTGTTCTAACAGGACGCGATAGACAGCTTTAAGSCGGAG 1212

QY 55 CysLysSerAlaGlyTyProGlyThrLeuIleProTyArgCysAspLeuSerAsnGlu 74
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1211 TTTGCAGAAACTTTTCCAAATCAACAGTTGGACTTTCTCTAGATGTCCGATATG 1152

QY 75 GluAspIleLeuSerMetPheSerAlaIleArgSerGlnHisSerGlyValAspIleCys 94
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1151 ACAATGGTAAAGACTGTCTGCTCTGATATTTAGAAACGATAGTGCAGATGACATCTG 1092

QY 95 IleAsnAsnAlaGlyLeuAlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrp 114
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1091 GTCATACAGCAGGACTGCTCTT-----GGCTTAGCTCCCTAT 1053

QY 115 LysAsp-----MetPheAsnValAsnValLeuAlaLeuSer 126
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1052 CAAGACTATGAAGAGTTGGATATGCTGACCATGTTGGATACCAATGTCAAAGGTTTGATG 993

QY 127 IleCysThrArgGluAlaTyArgGlnSerMetLysGluArgAsnValAspAspGlyHisIle 146
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 992 GCAGTCATCTGCTGTTCTTCCAGCAATGGTAAAGCCAT-----CAAGTCTATAT 939

QY 147 IleAsnIleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHisPheTy 166
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 938 ATCAATATGGGTCAACCGCAGGA-----ATTATGCTATGCTGCTGCAGCTGTTTAC 885

QY 167 SerAlaThrLysTyAlaValThrAlaLeuThrGluGlyLeuArgGlnLeuArgGlu 186
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 884 TCAGCCACCACCAAGCGGCGACTTAAAGCTTTTCAGATGGACTCGCA-----ATTGATACC 831

QY 187 AlaGlnThrHisIleArgAlaThrCysIleSerProGlyValValGluThrGlnPheAla 206
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 830 ATCGCAACGGATATCAAGTGTGAGCACCATTGACCTGGAAATGTGCAACACAGATTTTCT 771

QY 207 PheLysLeuHisAspLysAspProGluLysAlaAlaAlaThrTyGluGlnMetLysCys 226
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 770 ACAGTGGCTTTTCATGGTGATAAAGAACGAGCTGCGTGTTCACCAAGGAATAGAAGCT 711

QY 227 LeuLysProGluAspValAlaGluAlaValIleTyValLeuSerThrProAlaHisIle 246
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 710 TTGCAAGCTCAGGATATTGCAGATACAGTAGTCTATGTGACTAGTCAACCTCGTGTGT 651

QY 247 GlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 650 CAGATTACAGATGATGACCATTTATGGCAATCAACAGCGGCACA 609

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RESULT 5
US-09-453-702B-15
; Sequence 15, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Burland, Valerie
; Perna, Nicole T.
; Plunkett, Guy
; Welch, Rod
; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison

```

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; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B
; FILING DATE: 03-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95017
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6133
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-453-702B-15

Alignment Scores:
Pred. No.:      1.85e-31      Length:      6133
Score:          326.50       Matches:      85
Percent Similarity: 50.00%   Conservative: 43
Best Local Similarity: 33.20% Mismatches:      105
Query Match:     24.42%     Indels:        23
DB:              4          Gaps:          6

US-10-063-735-128 (1-260) x US-09-453-702B-15 (1-6133)

QY 7 GluArgTyrArgAspArgLeuAlaLeuValThrGlyAlaSerGlyGlyIleGlyAlaLa 26
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 651 GAGACGTAATGATGAAGTCAATTAATACCGCGCATCAAGTGTATTGGGAAGGT 710

QY 27 ValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGlyCysAlaArgThrValGly 46
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 711 ATTGCCAGAGAGCTTGGAAATGACAGGTGCAAAAGTTTACTGGGAGCACGACAGATTGAG 770

QY 47 AsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyrProGlyThrLeuIlePro 66
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 771 CGTATCGAAGCCATTGCAACACCGAAATTCGCCCGCAGGA-----GGAATTGCTAAAGCG 824

QY 67 TyrArgCysAspLeuSerAsnGluAspIleLeuSerMetPheSerAlaIleArgSer 86
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 825 CGGGAGTTGGATGTCACAGCCGACAGTCCATCGCGCGATTTCGTGCAAGCAGCGCTGGAT 884

QY 87 GlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeuAlaArgProAspThrLeu 106
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 885 AGCTGGGGCGAGTTGATGTTCTTATCAATAATGCGGGGTTATGCGCGCTTTTCACGCGTT 944

QY 107 LeuSerGlySerThrSerGlyTyrPlysAspMetPheAsnValAsnVal-----122
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 945 GCACAGGAAACAAAGATGATGGCGCTCATTGACGTGAATATCAAAAGGTGACTG 1004

QY 123 -----LeuAlaLeuSerIleCysThrArgGluAlaTyArgGlnSerMetLysGluArgAsn 140
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1005 TGGGGAATTGGCGCTGCTACTTCGGGTGATGGAAGCACACAGGTTCC-----1049

QY 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1050 -----GGTCAGATAATCAATCTTGTGTTCTTATTTGGTGCCTTTCTGTGTGCCACA 1100

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; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3 1/2 inch diskette
; COMPUTER: Dell Pentium
; OPERATING SYSTEM: MS DOS v6.22
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/487,429
; FILING DATE: 1995-06-07
; APPLICATION NUMBER: 08/426,787
; FILING DATE: 1995-04-21
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/487,429
; FILING DATE: 1995-06-07
; APPLICATION NUMBER: 08/426,787
; FILING DATE: 1995-04-21
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PB186P1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-610-5790
; TELEFAX: 310-309-8439
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
;
; US-09-643-990A-1
;
; Alignment Scores:
; Pred. No.: 7,17e-27 Length: 1830121
; Score: 322.50 Matches: 78
; Percent Similarity: 51.57% Conservative: 53
; Best Local Similarity: 30.71% Mismatches: 110
; Query Match: 24.12% Indels: 13
; DB: 4 Gaps: 6
;
; US-10-063-735-128 (1-260) x US-09-643-990A-1 (1-1830121)
;
; QY 7 GluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSerGlyGlyLeuAlaAla 26
; DB 1517820 GAAAAATGAAACTACTACTGATAGTAAAGTGAACGCGAGGCTTTGGCTGGCA 1517879
;
; QY 27 ValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGlyCysAlaArgThrValGly 46
; DB 1517880 ATCTGTAATAAATGATCGAAGCAGGCTATAAAGTGAATGGCAGCGGACGTCAGAT 1517939
;
; QY 47 AsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyrProGlyThrLeuIlePro 66
; DB 1517940 CGATTAGCAAGAAATCCATTACAAATTTGGCAAT-----AAATTTCTACCG 1517984
;
; QY 67 TyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMetPheSerAlaIleArgSer 86
; DB 1517985 CTTGGCTTTGACATTCGTGATGAACAGCCACCAATTAACGCTCTAAATACCTTCTCTGAA 1518044
;
; QY 87 GlnHisSerGlyValAspIleCysIleAsnAlaGlyLeuAlaArgPro---AspThr 105
; DB 1518045 GGCTGGCAAGCGGTGATTTATTAGTAATATGAGGTTTAGCTTGGGATTAGAGCG 1518104
;
; QY 106 LeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnValAsnValLeuAlaLeu 125
; DB 1518105 GCACATAAGCGGATTTACAGATTGGTATCATGATGATTACCAACATCAAGGATTG 1518164
;
; QY 126 SerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsnValAspAspGlyHis 145
; DB 1518165 GTTACTATCACTCGCTTGTGTGGCAATATGGTGGCTCGTAATAC-----GGGAG 1518218
;
; QY 146 IleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHisPhe 165
; DB 1518219 ATTATCAATTTGAGTTCAATTGCAGGT-----ACTTATCCTTATGACGAGCGTAATGTA 1518272
;
; QY 166 TyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeuArgGlnGluLeuArg 185
; DB 1518273 TATGTTGGAACATAAAGCTTTTGTACACAAATTTAGCTTAAATTTACGAGCGGATCTG--- 1518329
;
; QY 186 GluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyValVal---GluThrGln 204
; DB 1518330 ---GCAGCACAAAATTCGAGTAAGCAATGTTGAACCGGTTTATGTGGCGGTACGGAG 1518386
;
; QY 205 PheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaThrTyrGluGlnMet 224
; DB 1518387 TTCCTAATGTGCGCTTTTTCACGCGGATGATGAAAGAGCGCAAAAGTCTATGAAAACGCTG 1518446
;
; QY 225 LysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeuSerThrProAla 244
; DB 1518447 CAATCGGTTGAGCTGGAAGATATTGCGAAACATTTGATTATGCTTCATCAACACCTGAA 1518506
;
; QY 245 HisIleGlnIleGlyAspIleGlnMetArgProThrGluGln 258
; DB 1518507 CACGTGAACATTAATCGTATTGAGAGTAATGCCAACCGCTCAA 1518548
;
; RESULT 8
; US-09-221-017B-723
; Sequence 723, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Rose, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,017B
; FILING DATE: 23-DEC-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1182
; FILING DATE: 31-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1546
; FILING DATE: 30-JAN-1998
; APPLICATION NUMBER: PP2911
; FILING DATE: 09-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU98/01023
; FILING DATE: 10-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Montroy, Gladys H
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 27340-20021.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELE: 706141
; INFORMATION FOR SEQ ID NO: 723:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 763 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)

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; HYPOTHETICAL: NO
 ; ANTI-SENSE: UNKNOWN
 ; ORIGINAL SOURCE:
 ; ORGANISM: PORPHYROMONAS GINGIVALIS
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 1...763
 US-09-221-017B-723

Alignment Scores:

Pred. No.: 7,8e-32 Length: 763
 Score: 318.00 Matches: 85
 Percent Similarity: 52.48% Conservative: 42
 Best Local Similarity: 35.12% Mismatches: 105
 Query Match: 23.78% Indels: 10
 DBs: 4 Gaps: 7

US-10-063-735-128 (1-260) x US-09-221-017B-723 (1-763)

QY 16 ValThrGlyAlaSerGlyGlyLeuAlaValAlaValAlaValGlnGlnGly 35
 Db 3 ATCACCGGAGCACATCCGCATCGGTGCGCTCGCTGCGCTGGCATCGCTCGAT 62
 QY 36 LeuLysValValGlyCysAlaArgThrValGlyAsnIleGluGluLeuAlaGluCys 55
 Db 63 TATAACCTTATCATCACGGGACGCGCTCCGAACGTTTGCAGAAACATTCGCCATGAATC 122
 QY 56 LysSerAlaGlyTyrProGlyThrLeuLeuProTyrArgCysAspLeuSerAsnGluGlu 75
 Db 123 AGA---GCTGAATACCTGTGCAATCTCTCCGCTCTCTTTTCGATGTCGCAATCGCGAA 179
 QY 76 AspIleLeuSerMetPheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIle 95
 Db 180 GAAGTAGAGCCATTTCGGCAATTTCGCTGATCCTTGGCAGCGCTTTCGCTCTCGTG 239
 QY 96 AsnAsnAlaGlyLeuAlaArgPro---AspThrLeuLeuSerGlySerThrSerGlyTyr 114
 Db 240 AATAATGCGCGTTCGGCAGCGGACTCGACCCCATACAGTCGGTGACATTCAGACACTGG 299
 QY 115 LysAspMetPheAsnValAsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGln 134
 Db 300 GAACGTATGATAGACACCAATATCAAGGACTCTCTTACGTAACTCGCACCAATCAGCCCG 359
 QY 135 SerMetLysGluArgAsnValAspAspGlyHisIleIleAsnIleAsnSerMetSerGly 154
 Db 360 GGTATGATAGCCGAGCGCC-----GGCATATCATCAATATCGGTCTATTGCCCGC 413
 QY 155 HisArgValLeuProLeuSerValThrHisPheTyrSerAlaThrLysTyrAlaValThr 174
 Db 414 AAGGAAGTT-----TACTCTAAACGCAATGCTATTGTGTCACGACGATGCCGTAGAT 467
 QY 175 AlaLeuThrGluGlyLeuArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThr 194
 Db 468 GCTCTTCGAAAGCGATCGGTATAGATATG-----CTTCTTATGGCATCAAAAGTCACA 521
 QY 195 CysIleSerProGlyValValGluThrGlnPheAlaPhe---LysLeuHisAspLysAsp 213
 Db 522 CAGATTTCGCGAGCAGTGGAGCGAGTTCGCTGGTGGCTTCATGAT---GAT 578
 QY 214 ProGluLysAlaAlaAlaThrTyrGluGlnMetLysCysLeuLysProGluAspValAla 233
 Db 579 CAGGCCAAGCGCGATCGCTGTACAAAGGCTTCACTCTCTCTGTGCGCAACGACATAGCG 638
 QY 234 GluAlaValIleTyrValLeuSerThrProAlaHisIleGlnIleGlyAspIleGlnMet 253
 Db 639 GAGTGTATGCGCGCTACTGAACCTGCTGATAATATCTGTATCAACGATATGCTGTC 698
 QY 254 ArgPro 255
 Db 699 ATGCCG 704

RESULT 9

US-09-328-352-2199

; Sequence 2199, Application US/09328352
 ; Patent No. 6562958
 ; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 ; FILE REFERENCE: GTC99-03PA
 ; CURRENT APPLICATION NUMBER: US/09/328,352
 ; NUMBER OF SEQ ID NOS: 8252
 ; SEQ ID NO 2199
 ; LENGTH: 798
 ; TYPE: DNA
 ; ORGANISM: Acinetobacter baumannii
 US-09-328-352-2199

Alignment Scores:

Pred. No.: 1,14e-31 Length: 798
 Score: 317.00 Matches: 87
 Percent Similarity: 51.00% Conservative: 41
 Best Local Similarity: 34.66% Mismatches: 107
 Query Match: 23.71% Indels: 16
 DBs: 4 Gaps: 8

US-10-063-735-128 (1-260) x US-09-328-352-2199 (1-798)

QY 13 LeuAlaLeuValThrGlyAlaSerGlyGlyLeuGlyAlaValAlaValAlaArgAlaLeuVal 32
 Db 43 TTAGCATTTAGTTACAGGCGCATCAGCAGGTTTGGTTATAGTATTTCAAAAAACTGATT 102
 QY 33 GlnGlnGlyLeuLysValValGlyCysAlaArgThrValGlyAsnIleGluGluLeuAla 52
 Db 103 GAGTCAGGCTATAAAGTTATTGGATGTGGAAGCGCGAGAAAAAATTAGAGAACTACAA 162
 QY 53 AlaGluCysLysSerAlaGlyTyrProGlyThrLeuIleProTyrArgCysAspLeuSer 72
 Db 163 AAACAGCTTGGCGAAAATTTCTACCCACTCGTATTT-----GATATGACT 207
 QY 73 Asn---GluGluAspIleLeuSerMetPheSerAlaIleArgSer-----GlnHisSer 89
 Db 208 GATACGGCAGAAAAATATAAATAAGTTATTTAAAGAAATTTACCAATGAAATTTCAATCGAT 267
 QY 90 GlyValAspIleCysIleAsnAsnAlaGlyLeuAlaArgPro---AspThrLeuLeuSer 108
 Db 268 CAATTTGACTTACTAGTGAATAATGCAAGGCTTGGCATTTGGCTTAGAGCCAGCATAAA 327
 QY 109 GlySerThrSerGlyTyrLysAspMetPheAsnValAsnValLeuAlaLeuSerIleCys 128
 Db 328 GCGGATTTAGATGATTGGTACACCATGATTCATACCAATGTTAAAGGCTTGTTCACGGTT 387
 QY 129 ThrArgGluAlaTyrGlnSerMetLysGluArgAsnValAspAspGlyHisIleIleAsn 148
 Db 388 ACCCGATTAAATTTTACCAAGTATGTTAAAGAGAAA-----TCAGGCTTAATCATTAAT 441
 QY 149 IleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHisPheTyrSerAla 168
 Db 442 ATGGTTCAATTCGAGGT-----ACATACCATATCCAGGTGGTAAATGTATATATGGGCA 495
 QY 169 ThrLysTyrAlaValThrAlaLeuThrGluGlyLeuArgGlnGluLeuArgGluAlaGln 188
 Db 496 ACAAAAGCTTTGTAGAGCAGCTTTAGTTTAAATCTACGTGCAGATTG-----GCTGGT 549
 QY 189 ThrHisIleArgAlaThrCysIleSerProGlyValVal---GluThrGlnPheAlaPhe 207
 Db 550 ACTGGCTGCGGGTAAACGAATATTGAGCCAGGGTTGTGTGGTGTACCGAATTTTCTCTT 609
 QY 208 LysLeuHisAspLysAspProGluLysAlaAlaAlaThrTyrGluGlnMetLysCysLeu 227
 Db 610 GTACGTTTTAAGGAGATCAGGAGAAAGCTTAACAGTCTATACGATAAGAAAAATCCAATT 669
 QY 228 LysProGluAspValAlaGluAlaValIleTyrValLeuSerThrProAlaHisIleGln 247
 Db 670 TTGCCGGAAGATATTGCAATATACAGTAGCATGGATCGCATCACAAACCCGATATTAAAT 729

Qy	152	MetSerGlyHisArgValLeuProLeuSerValThrHisPheTyrSerAlaThrLysTyr	171
Db	472	ACGCGAGGCAGC-----TGCCCTTACGCCGCGGAAACGCTCATGGGCGACCAAGCC	525
Qy	172	AlaValThrAlaLeuThrGluGlyLeuArgGlnGluLeuArgGluAlaGlnThrHisIle	191
Db	526	TTTGTCGCTCAGTTTAGCTCAATCTTCGTACCGACCTGCAC-----GGCACCCGCGTG	579
Qy	192	ArgAlaThrCysIleSerProGlyValVal---GluThrGlnPheAlaPheLysLeuHis	210
Db	580	CGCGTAGCCAGACATCGAGCCGGGCTCTGTGGCGGCACCGGATTTTCTAACGTCGCGCTT	639
Qy	211	AspLysAspProGluLysAlaAlaAlaThrTyrGluGlnMetLysCysLysLysProGlu	230
Db	640	AAGGGCGATGACGCTAAAGCCGAAAGACCTTACGAAATAACCGAGCGCTAACGCCGGA	699
Qy	231	AspValAlaGluAlaValIleTyrValLeuSerThrProAlaHisIleGlnIleGlyAsp	250
Db	700	GATGTGACCGAGCGGGTCTGTTGGTGCACCCTGCCGGAACATGTCAACATCAACACC	759
Qy	251	IleGlnMetArgProThrGluGln	258
Db	760	CTGGAGATGATGCCGGTCAGTCAG	783

RESULT 12

US-09-385-028-22/c
Sequence 22, Application US/09385028
Patent No. 6232106
GENERAL INFORMATION:
APPLICANT: Susan E. Jensen
APPLICANT: Keamena A Aidoo
APPLICANT: Ashish S. Paradkar
TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
Patent No. 6232106
TITLE OF INVENTION: Acid Biosynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN PPLC
STREET: The Jenner Building, 400 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,028
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: D. Douglas Price
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418/P57452US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEFAX: (202) 39305350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 744 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-385-028-22

Alignment Scores:					
Pred. NO.:	1.52e-30	Length:	744		
Score:	308.00	Matches:	78		
Percent Similarity:	51.41%	Conservative:	50		
Best Local Similarity:	31.33%	Mismatches:	111		
Query Match:	23.04%	Indels:	10		
DB:	3	Gaps:	5		
US-10-063-735-128 (1-260) x US-09-385-028-22 (1-744)					
QY	12	ArgLeuAlaLeuValThrGlyValSerCysGlyGlyIleGlyAlaValAlaAraGlaLeu	31		
Db	723	AAGTCGGCTCATCGGGCGCAGATCGGCATCGCGAGGCCACGCCGCCGCTTG	664		
QY	32	ValGlnGlnGlyLeuLysValValGlyCysAlaArgThrValGlyAsnIleGluGluLeu	51		
Db	663	CCGCCGAGGGCGCGGTGGCCATCCCGCGCGCCGGTGCAGAAGTGGCGGCCCTG	604		
QY	52	AlaAlaGlyCysLysSerAlaGlyTyProGlyThrLeuIleProTyArgCysAspLeu	71		
Db	603	GGTGACGAGTCAACCGCGCGGGCGGAAGTCCATGTCTCTCTCTCTCTCTCTCT	550		
QY	72	SerAsnGluGluAspIleLeuSerMetPheSerLalleArgSerGlnHisSerGlyVal	91		
Db	549	GCCGACGGGCGGGGTGGACGCCCGCTCCCTCCACCGTCGAGCGGTGGCGGCTC	490		
QY	92	AspIleCysIleAsnAsnAlaGlyLeuAlaArgProAspThrLeuLeuSerGlySerThr	111		
Db	489	GACATCTCTGTAACACGCGGAGTATCATGTCTGGCCCGGTGGAGAGCGCGACACC	430		
QY	112	SerGlyTrpLysAspMetPheAsnValAsnValLeuAlaLeuSerIleCysThrArgGlu	131		
Db	429	ACCGACTGACCGGATGATCGACACCAATCTCTGGGCTGTATGATGACCCGGGGG	370		
QY	132	AlaTyrglnSerMetLysGluArgAsnValAspAspGlyHisIleIleAsnIleAsnSer	151		
Db	369	GCCTCTCCCCATCTGTCGCG-----AGCAAGGCGCACCGTGTGCAGATGCTCTCG	319		
QY	152	MetSerGlyHisargValLeuProLeuSerValThrHisPheTyrsSerAlaThrLysTy	171		
Db	318	ATCGGGGCGCG-----GTGAACGTCCGCAACGCGCGCTCTACCGCCACGAAAGTTC	265		
QY	172	AlaValThrAlaLeuThrGluGlyLeuArgGlnGluLeuArgGluAlaGlnThrHisIle	191		
Db	264	GGTGTGAACGCTTCAGCGAGACGCTCGCCACGAGGTCACCGAG-----CGCGGGGTG	211		
QY	192	ArgAlaThrCysIleSerProGlyValValGluThrGlnPheAlaPheLysLeu---His	210		
Db	210	CGGGTCTGTCTATCGAGCGGGGCACCGCACACGAGGTGCGCGGCCACATACCCAC	151		
QY	211	AspLysAspProGlnLysAlaAlaAlaThrTyrglnMetLysCysLeuLysProGlu	230		
Db	150	ACCGCCACCMAGAGATGTACGAGCGGATCAGCCAGTCCGCAAGTCCAGCGCCCGAG	91		
QY	231	AspValalaGluAlaValIleTyrrValLeuSerThrProAlaHisIleGlnIleGlyAsp	250		
Db	90	GACATCGGAGGCGGTCCGCTACGCGGTGACCGCGCGCACACCGGACCGTCCACGAG	31		
QY	251	IleGlnMetArgProThrGluGlnVal	259		
Db	30	ATCTTTATACGCCCCCACCGACCAAGTTC	4		

RESULT 13

```

RESOLUTION 13
US-09-726-614-22/c
; Sequence 22, Application US/09726614
; Patent No. 6514735
; GENERAL INFORMATION:
; APPLICANT: Susan E. Jensen
; APPLICANT: Kwamena A Aidoo
; APPLICANT: Ashish S. Paraskar
; TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
; Patent No. 6514735
; TITLE OF INVENTION: Acid Biosynthesis
;

```

```

; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN,PPLC
; STREET: The Jennifer Buliding, 400 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/726,614
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/790,462
; FILING DATE: 29-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: D. Douglas Price
; REGISTRATION NUMBER: 24,514
; REFERENCE/DOCKET NUMBER: 1418/P57452US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202 638-6666
; TELEFAX: (202) 39305350
; TELEX: RCA 248593 IDEA UR
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 744 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-726-614-22

Alignment Scores:
Pred. No.: 1.52e-30 Length: 744
Score: 308.00 Matches: 78
Percent Similarity: 51.41% Conservative: 50
Best Local Similarity: 31.33% Mismatches: 111
Query Match: 23.04% Indels: 10
DB: 4 Gaps: 5

US-10-063-735-128 (1-260) x US-09-726-614-22 (1-744)

Qy 12 ArgLeuAlaLeuValThrGlyAlaSerGlyGlyleGlyAlaAlaValAlaArgAlaLeu 31
Db 723 AAAGTCGGCTCATCGCGCGGAGTCCGGGCATCGCGGAGGCCACGCCGCCGCGCTG 664

Qy 32 ValGlnGlnGlyLeuLysValValGlyCysAlaArgThrValGlyAsnIleGluGluLeu 51
Db 663 GCCGCCGAGGCGCGCGCGTGCCATCGCGCGCGCGGTGAGAAGCTGCGCGCGCTG 604

Qy 52 AlaAlaGluCysLysSerAlaGlyTyrProGlyThrLeulleProTyrzArgCysAspLeu 71
Db 603 GGTCAGCAGTGCACCGCGCGCGCGGAAGTCCATGTCCTC-----GAATCGACGTC 550

Qy 72 SerAsnGluGluAspIleLeuSerMetPheSerAlaIleAArgSerGlnHisSerGlyVal 91
Db 549 GCCGACCGGAGGGGTGGACCGCGCGTCCGCTCCACCGTCGAGCGGCTGGCGGCTC 490

Qy 92 AspIleCysIleAsnAlaGlyLeuAlaArgProAspThrLeuLeuSerGlySerThr 111
Db 489 GACATCTCTCAACAACCGCGGATCATCTGCTCGCGCGCGTGTGAGGACGCCGACACC 430

Qy 112 SerGlyTrpLysAspMetPheAsnValAsnValLeuAlaLeuSerIleCysThrArgGlu 131
Db 429 ACCGACTGGACCCGGATGATCGACCACTCTCTGGCGCTGATGTACATGACCCCGGCG 370

Qy 132 AlatyTrpSerMetLysGluArgAsnValAspAspGlyHisIleIleAsnSer 151

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Db 10619 ATCTTCATACGCCCCCACCAGGTC 10593

Search completed: September 16, 2004, 17:59:02
Job time : 1112 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2004, 11:18:21 ; Search time 115 Seconds

(without alignments)
713.346 Million cell updates/sec

Title: US-10-063-735-128

Perfect score: 1337

Sequence: 1 MARPGMRWRDLALVTGAS.....STPAHIQIGDIOMRTEQVT 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SEPTREMBL_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	932	69.7	181	4	Q9BUC7	Q9buc7 homo sapien
2	924	69.1	181	4	Q9H674	Q9h674 homo sapien
3	864	64.6	181	11	Q8R249	Q8r249 mus musculus
4	482	36.1	251	5	Q9VYU9	Q9vyu9 drosophila
5	476	35.6	246	5	Q9VMH9	Q9vmh9 drosophila
6	442.5	33.1	250	5	Q9VZ19	Q9vz19 drosophila
7	441.5	33.0	250	5	Q8SY92	Q8sy92 drosophila
8	440	32.9	251	5	Q9XYM2	Q9xym2 drosophila
9	418.5	31.3	250	5	Q9VDC0	Q9vdc0 drosophila
10	407.5	30.5	248	5	Q9VD30	Q9vd30 drosophila
11	387.5	29.0	266	5	Q9VU92	Q9vu92 drosophila
12	380.5	28.5	200	5	Q95T88	Q95t88 drosophila
13	379	28.3	249	5	Q9IRN0	Q9irn0 drosophila
14	377	28.2	249	5	Q9SR56	Q9sr56 drosophila
15	375	28.0	256	16	Q8AAQ5	Q8aaq5 bacteroides
16	368	27.5	257	16	Q8YZ15	Q8yz15 anabaena sp

17	363	27.2	258	16	Q83BJ5	Q83bj5 coxiella bu
18	355.5	26.6	273	16	Q9JUV3	Q9juv3 neisseria m
19	353.5	26.4	273	16	Q9JZR8	Q9jzr8 neisseria m
20	353	26.4	231	16	Q8NUV9	Q8nuv9 staphylococ
21	351	26.3	231	16	Q99RE5	Q99rf5 staphylococ
22	349.5	26.1	240	16	Q92X14	Q92xi4 rhizobium m
23	348.5	26.1	255	1	O34187	O34187 halobacteri
24	345	25.8	259	16	Q8FNO0	Q8fng0 corynebacte
25	336.5	25.2	253	16	Q83RE8	Q83re8 shigella fl
26	335.5	25.1	248	16	Q7UCH2	Q7uch2 shigella fl
27	334.5	25.0	244	16	Q8YV39	Q8yv39 anabaena sp
28	334.5	25.0	253	16	Q8FHD2	Q8fhd2 escherichia
29	332	24.8	249	16	Q93OM2	Q93om2 rhizobium m
30	331.5	24.8	271	16	Q8UH28	Q8uh28 agrobacteri
31	331	24.8	245	16	Q82ZU1	Q82zu1 enterococcu
32	331	24.8	248	16	Q88T73	Q88t73 lactobacill
33	328.5	24.6	248	16	Q8X505	Q8x505 escherichia
34	328.5	24.6	269	2	Q838D4	Q838d4 mycobacteri
35	327	24.5	248	2	Q9RH22	Q9rhd2 zymomonas m
36	326.5	24.4	253	16	Q97NV2	Q97nv2 streptococc
37	326	24.4	264	16	Q81M93	Q81m93 bacillus an
38	325.5	24.3	240	16	Q8X6K1	Q8x6k1 escherichia
39	325.5	24.3	260	17	Q9HSR4	Q9hsr4 halobacteri
40	324.5	24.3	249	2	Q9AGD6	Q9agd6 yersinia ps
41	323.5	24.2	244	16	Q55922	Q55922 synechocyst
42	323	24.2	239	16	Q87GP0	Q87gp0 vibrio para
43	322.5	24.1	230	16	Q8CN40	Q8cn40 staphylococ
44	321.5	24.0	245	16	Q9RJL6	Q9rjl6 streptomyce
45	320.5	24.0	249	2	Q93AP1	Q93ap1 yersinia ps

ALIGNMENTS

RESULT 1

Q9BUC7 PRELIMINARY; PRT; 181 AA.

AC Q9BUC7; ID Q9BUC7; PRT; 181 AA.

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Uterus;

RA Strausberg R.;

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.

DR EMBL: BC002731; AAH02731.1; -

DR GO: GO:0016491; P:oxidoreductase activity; IEA.

DR GO: GO:0008152; P:metabolism; IEA.

DR InterPro: IPR002198; ADH short.

DR Pfam: PF00106; adh short; 1.

DR PRINTS: PR00080; SDRFAMILY.

DR PROSITE: PS00061; ADH_SHORT; 1.

KW Hypothetical protein; Oxidoreductase.

SQ SEQUENCE 181 AA; 20022 MW; 5BFCE5727835A38 CRC64;

Query Match 69.7%; Score 932; DB 4; Length 181;

Best Local Similarity 100.0%; Pred. No. 2.1e-70;

Matches 181; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 MFSAIRSOHSGVDICINNAGLARPDTLLSGTSGWKDMFNVLALSICTREAYQSMKER 139

Db 1 MFSAIRSOHSGVDICINNAGLARPDTLLSGTSGWKDMFNVLALSICTREAYQSMKER 60

Qy 140 NVDDGHILININSGHVRVLPSTVTHFYATKAVYALTTEGLROELREAQTHIRATCISPG 199

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Db 61 NVDDGHIINSMGHRVLPVSVTHFYSAKYAVTALTEGLRQELREAQTHIRATCISPG 120
Qy 200 VVETQFAFKLHDKDPEKAAATYEQMKLKPEDVAEAVIYVLTSTPAHIQIGDIQMRPTEQV 259
Db 121 VVETQFAFKLHDKDPEKAAATYEQMKLKPEDVAEAVIYVLTSTPAHIQIGDIQMRPTEQV 180
Qy 260 T 260
Db 181 T 181

RESULT 2
Q9H674 PRELIMINARY; PRT; 181 AA.
AC Q9H674;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein FLJ22543.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RA Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
RA Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
RA Nakamura Y., Isoigai T., Sugano S.;
RT "NEDO human cDNA sequencing project."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; AK026196; BAB15390.1; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
KW Hypothetical protein; Oxidoreductase.
SQ SEQUENCE 181 AA; 19962 MW; 4EFCAB58978CE59D CRC64;

Query Match 69.1%; Score 924; DB 4; Length 181;
Best Local Similarity 99.4%; Pred. No. 9.9e-70;
Matches 180; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 80 MFSAIRSQHSGVDICINNAGLARPDTLTSGSTSGWKDMFNVLALSICTREAYQSMKER 139
Db 1 MFSAIRSQHSGVDICINNAGLARPDTLTSGSTSGWKDMFNVLALSICTREAYQSMKER 60

Qy 140 NVDDGHIINSMGHRVLPVSVTHFYSAKYAVTALTEGLRQELREAQTHIRATCISPG 199
Db 61 NVDDGHIINSMGHRVLPVSVTHFYSAKYAVTALTEGLRQELREAQTHIRATCISPG 120

Qy 200 VVETQFAFKLHDKDPEKAAATYEQMKLKPEDVAEAVIYVLTSTPAHIQIGDIQMRPTEQV 259
Db 121 VVETQFAFKLHDKDPEKAAATYEQMKLKPEDVAEAVIYVLTSTPAHIQIGDIQMRPTEQV 180

Qy 260 T 260
Db 181 T 181

RESULT 3
Q8R249 PRELIMINARY; PRT; 181 AA.
AC Q8R249;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to hypothetical protein MGC4172.
OS Mus musculus (Mouse).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR EMBL; BC022224; AAH22224.1; -.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH_short.
DR Pfam; PF00106; adh_short; 1.
KW Hypothetical protein; Oxidoreductase.
SQ SEQUENCE 181 AA; 19984 MW; 0791543F571EA43B CRC64;

Query Match 64.6%; Score 864; DB 11; Length 181;
Best Local Similarity 90.6%; Pred. No. 1.1e-64;
Matches 164; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

Qy 80 MFSAIRSQHSGVDICINNAGLARPDTLTSGSTSGWKDMFNVLALSICTREAYQSMKER 139
Db 1 MFSAIRSQHSGVDICINNAGLARPDTLTSGSTSGWKDMFNVLALSICTREAYQSMKER 60

Qy 140 NVDDGHIINSMGHRVLPVSVTHFYSAKYAVTALTEGLRQELREAQTHIRATCISPG 199
Db 61 NIDGHIINSMGHRVPSVTHFYSAKYAVTALTEGLRQELREAQTHIRATCISPG 120

Qy 200 VVETQFAFKLHDKDPEKAAATYEQMKLKPEDVAEAVIYVLTSTPAHIQIGDIQMRPTEQV 259
Db 121 LVETQFAFKLHDKDPEKAAATYEHKLPEDVAEAVIYVLTSTPHVQVGDIQMRPTEQV 180

Qy 260 T 260
Db 181 T 181

RESULT 4
Q9VYU9 PRELIMINARY; PRT; 251 AA.
AC Q9VYU9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG9360 protein (RH17287p).
GN CG9360.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RX MEDLINE=20196006; PubMed=107311132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter B.G., Helt J., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
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[illegible]

QY	66	PYRCDLSNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLLSGS-TSGWKDMFNVNLA	124
Db	60	PRRCDVSKEDQVQSSFDWIERLEGADVLLNAGITRETETELVTPNTQKLKEVIDTNVWG	119
QY	125	LSICTREAYQSMKERNVDGHHIININSMGHRVL-----PLSVTHFYSATKYAVTALTEGL	180
Db	120	VIVCTREAFNMKRG-GEHVLINISAGHQVLNFIDVLPFSNIYPATKAITAITETY	178
QY	181	ROELREAQTHIRATCISPGVETQFAFKLHDKPEKAAATYEQMKCLKPEDVAEAVIYVL	240
Db	179	ROEQLHNSKIRVTCIGCAVNTNIF-----PEEIHFYKDMARLEPANIADAVMAL	231
QY	241	STPAHIQIGDI	251
Db	232	ATPPHVQVSI	242
RESULT 6			
ID	Q9VZ19	PRELIMINARY;	PRT; 250 AA.
AC	Q9VZ19;		
DT	01-MAY-2000 (TReMBLrel. 13, Created)		
DT	01-MAY-2000 (TReMBLrel. 13, Last sequence update)		
DT	01-JUN-2003 (TReMBLrel. 24, Last annotation update)		
DE	ANTDH protein.		
GN	ANTDH OR CG1386.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Berkley;		
RX	MEDLINE=20196006; PubMed=10731132;		
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,		
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,		
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,		
RA	Sutcliffe G.G., Wortman J.R., Yandell M.D., Zhang L.X.,		
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,		
RA	Abel J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Balgwin D.,		
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,		
RA	Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,		
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,		
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,		
RA	Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,		
RA	de Fabios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,		
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,		
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,		
RA	Foster K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,		
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,		
RA	Harris D., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,		
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,		
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,		
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,		
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,		
RA	Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,		
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,		
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,		
RA	Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., M.G.,		
RA	Pallazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,		
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,		
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,		
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,		
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,		
RA	Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,		
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,		
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,		
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,		
RA	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;		
RT	"The genome sequence of Drosophila melanogaster."		

RL	Science 287:2185-2195(2000).		
CC	-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES		
CC	(SDR) FAMILY.		
CC	EMBL; AE003485; AAF48012.1; -.		
DR	FlyBase; FBgn0026268; antdh.		
DR	GO; GO:0016491; P:oxidoreductase activity; IEA.		
DR	GO; GO:0008152; P:metabolism; IEA.		
DR	InterPro; IPR002198; ADH_short.		
DR	Pfam; PF00106; adh_short; 1.		
DR	PRINTS; PR00080; SDRFAMILY.		
KW	Oxidoreductase.		
SQ	SEQUENCE 250 AA; 27279 MW; 790E8F1DCADF025 CRC64;		
Query Match 33.1%; Score 442.5; DB 5; Length 250;			
Best Local Similarity 36.5%; Pred. No. 4.2e-29;			
Matches 93; Conservative 56; Mismatches 91; Indels 15; Gaps 5;			
QY	6	MERWRDLRLALVTGASGGIGAAVARALVQOQGLKVGVCARTVGNIELAAECKSAGYPTLI	65
Db	1	MERWQNRVAVVTGASSGIGSAIAKDLVLAGTVVGLARRVDRVKELQREL-PAEKRGKLF	59
QY	66	PYRCDLSNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLLSGSTSGWKDMFNVNLA	125
Db	60	ALYCDVGNESVNEAFDWIIQKLGALDVLVNNAGTLQPGYLVDMPAVNQVLQTNIMGI	119
QY	126	SICTREAYQSMKERNVDGHHIININSMGHRVPLSV-----THFYSATKYAVTALTEGL	180
Db	120	VICTQRAVRSMRERKF-DGHVVLINSLCHKTMTATEGVADPVNVVYPSKHAVALAEGY	178
QY	181	ROELREAQTHIRATCISPGVETQFAFKLHDKPEKAAATYEQMKCLKPEDVAEAVIYVL	240
Db	179	ROEQLHNSKIRVTCISVSPGVDTIV-----PDSIREAIKD-RMLHSEDIAGQGLVYAI	230
QY	241	STPAHIQIGDIQMRP	255
Db	231	ATPPHVQVHELIIP	245
RESULT 7			
Q9SY92	PRELIMINARY;	PRT; 250 AA.	
ID	Q9SY92;		
DT	01-JUN-2002 (TReMBLrel. 21, Created)		
DT	01-JUN-2002 (TReMBLrel. 21, Last sequence update)		
DT	01-JUN-2003 (TReMBLrel. 24, Last annotation update)		
DE	RH21971p.		
GN	ANTDH OR CG1386.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=Berkley;		
RA	Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,		
RA	Champe M., Chavez C., Dorsett V., Drensek D., Farfan D., Frise E.,		
RA	George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,		
RA	Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,		
RA	Patel S., Phuananavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,		
RA	Celniker S.;		
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.		
CC	-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES		
CC	(SDR) FAMILY.		
DR	EMBL; AY071705; AAL49327.1; -.		
DR	FlyBase; FBgn0026268; antdh.		
DR	GO; GO:0016491; P:oxidoreductase activity; IEA.		
DR	GO; GO:0008152; P:metabolism; IEA.		
DR	InterPro; IPR002198; ADH_short.		
DR	Pfam; PF00106; adh_short; 1.		
DR	PRINTS; PR00080; SDRFAMILY.		
KW	Oxidoreductase.		
SQ	SEQUENCE 250 AA; 27265 MW; 6B8C78F1DCB2BF25 CRC64;		

[illegible]

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RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (DRC-2001) to the ENBL/GenBank/DBJ databases.
CC -I- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR ENBL; AE003734; AAF55877.1; -.
DR ENBL; AY069036; AAL39181.1; -.
DR FlyBase; FBgn0038878; CG3301.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
KW Oxidoreductase.
SQ SEQUENCE 250 AA; 27236 MW; 8C6892AFC62C4DF5 CRC64;
Query Match 31.3%; Score 418.5; DB 5; Length 250;
Best Local Similarity 38.2%; Pred. No. 4.3e-27;
Matches 99; Conservative 50; Mismatches 87; Indels 23; Gaps 6;
QY 6 MERWRDLALVTGASGGTGAARALVQOGLKVGVCARTVGNIEELAAECKS---AGYGP 62
DB 1 MNRMLNVAVTGASAGIGAACCRDLVAKGMVVGGLARR-----EKVLQDIKSSLPADQAA 56
QY 63 TLIPFYCDLSNEEDILSMFSAIRSOHSGVDICINNAGLARPDTLISGSTSG-WKDMFNVN 121
DB 57 RFHTRPCDVNSQVQVITDFAWIDRTLGGADVLVNNAGIIRQWNTDPNSADVRAILDVN 116
QY 122 VLALSICTREAVQSMKERNVDDGHIININSMGHRVPLS--VTHFYSATKYAVTALTEG 179
DB 117 VLGVTWCTQRWLSLQRKQVNDGHVNVSVGVHVPAGEFSLNMYAPSKHAIITALTEI 176
QY 180 LRQELREAQTHIRATCISPGVVEVTOFAFKLHDKDPEKAAATVEQ---MKCLKPDEVAEAV 236
DB 177 LRQEFPIKGTQTKITSISFGVATEIF-----EAGSWEQTPGMPMLRSEDIADAV 226
QY 237 IYVLSTPAHIQIGDIQMP 255
DB 227 TYCIQTPTPTVQIKELIIRP 245
RESULT 10
Q9VD30 PRELIMINARY; PRT; 248 AA.
AC Q9VD30;
ID Q9VD30;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CG7077 protein (GH05294p).
GN CG7077.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Fandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brockner P., Brothier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
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RA Durbin K.J., Evangelista C.C., Ferraz C., Perriera S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mepherston D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RC Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JUN-2002) to the ENBL/GenBank/DBJ databases.
CC -I- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
CC (SDR) FAMILY.
DR ENBL; AE003738; AAF55973.1; -.
DR ENBL; AY119471; AAM50125.1; -.
DR HSP; P14061; 1A27.
DR FlyBase; FBgn0038946; CG7077.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH short.
DR Pfam; PF00106; adh_short; 1.
DR PRINTS; PR00080; SDRFAMILY.
KW Oxidoreductase.
SQ SEQUENCE 248 AA; 27265 MW; FDF1AF7C37155A70 CRC64;
Query Match 30.5%; Score 407.5; DB 5; Length 248;
Best Local Similarity 37.6%; Pred. No. 3.6e-26;
Matches 97; Conservative 50; Mismatches 86; Indels 25; Gaps 6;
QY 9 WRDLALVTGASGGTGAARALVQOGLKVGVCARTVGNIEELAAECKSAGYPTLIPYR 68
DB 7 WRNKVAVVTGASVGIGATTATIELANAGMVVGLARRVELIELARDQVTGV---GKIFARQ 63
QY 69 CDLSNEEDILSMFSAIRSOHSGVDICINNAGLARPDTLISGSTSGWKDMFNVNIALSLIC 128
DB 64 CDLNDEEQALSAFNWIREKFOAIHVLIICNAGLIKANFLSESPTKIKELFDNNVATASC 123
QY 129 TREAYQSMKERNVDDGHIININSMGHRV--LPLSVTHFYSATKYAVTALTEGLRQELRE 186
DB 124 LREALKHAARKV-RGHIVVWNSVLGHRIPVPEVPLFVSVPATKHAITALCQTVRQEIHF 182
QY 187 AQTHIRATCISPGVVEVTOFAFKLHDKDPEKAAATVEQ-----MKCLKPDEVAEAVILST 242
DB 183 LKLNKILKLSICPGMVDTFD-----LSVYSQVAELPKLQARDVAKAVIALYALT 230
QY 243 PAHIQIGDI---QMPTE 257
DB 231 PDGVQVEDILIQOMRKVD 248
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5

Db 175 LEVIRQELRGFKTKIKVT 192

RESULT 13

Q8IRNO PRELIMINARY; PRT; 249 AA.

AC Q8IRNO;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE CG7090-PB

GN CG10962 OR CG7090.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

SEQUENCE FROM N.A.

RP MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers J.H., Blazey R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,

RA Ball J.F., Agbayani A., An H.J., Andrews-Frankoch C., Balowin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,

RA Burtis K.C., Buesam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Foeiser C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Keichum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,

RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,

RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,

RA Williams S.M., Woodgett J., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.H.O.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster."

RL Science 287:2185-2195(2000).

RN [2]

SEQUENCE FROM N.A.

RP Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,

RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

RA Banzon J., An H., Baldwin D., Banzon K.Y., Buesam D.A.,

RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,

RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

RA Ibegwam C., Jalali M., Kruse D., Li P., Mattel B., Moshrefi A.,

RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,

RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

RA Phaulanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

RA Shouanenavong S., Strong R., Svirkas R., Tector C., Tyler D.,

RA Stapleton M., Strong R., Svirkas R., Tector C., Tyler D.,

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA

Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

RT "Sequencing of Drosophila melanogaster genome."

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [3]

SEQUENCE FROM N.A.

RP Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,

RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,

RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,

Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,

RA Kronmiller B., Marshall B., Milburn G., Richter J., Russo S.,

RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,

RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;

RT "Annotation of Drosophila melanogaster genome."

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [4]

SEQUENCE FROM N.A.

RP Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter J.C.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [5]

SEQUENCE FROM N.A.

RP FlyBase;

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE003445; AAF6428.1; -

DR FlyBase; FBgn0030073; CG10962.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR002198; ADH short.

DR Pfam; PF00106; adh short; 1.

DR PRINTS; PRO0080; SDRFAMILY.

DR SQ SEQUENCE 249 AA; 27141 MW; 8DAD823CEB7319AF CRC64;

Query Match 28.3%; Score 379; DB 5; Length 249;

Best Local Similarity 35.8%; Pred. No. 8.9e-24;

Matches 92; Conservative 55; Mismatches 88; Indels 22; Gaps 7;

Qy 6 MEMRDRLALVTGSGGIGAAVARALVQOGLKVVGVCARTVGTIEE-----LAAECKSAGYP 61

Db 1 MDRQNEVAVISGASSGIGAACRLVVAAGLVQVGLARRDRLEQLRQSLPAEQRMRFH- 59

Qy 62 GTLLPYRCDSLNEEDILSMFSAIRSQHSQVDICINNAGLARPTLLSGSTSGWKMDNFVN 121

Db 60 ----QHKCDVSQELQVDTAFETWIEKEGLGIDVLINNAGIVLGGQLIDMPTKDINNILQTN 115

Qy 122 VLALISICTRAYQSKERNVDDGHIININS---MSGHRVLPISVT-HFYSATKYAVTALT 177

Db 116 LMGSIIYCTKLAASSMRRQV-AGHLIFVNSTAGVAGYKPPADESLNAYTFSKFLTAIVQ 174

Qy 178 EGLRQELREAOHTIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVI 237

Db 175 EICQELINQSKIKTTSINPGWATEIV-----PDETAKLGEV-ILQADDDVAQVL 226

Qy 238 YVLSTPAHIQIGDIQMR 254

Db 227 YALSTPPHTQVEQITLR 243

RESULT 14

Q95R56 PRELIMINARY; PRT; 249 AA.

AC Q95R56;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE SD06635P.

GN CG10962 OR CG7090.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

SEQUENCE FROM N.A.

RP Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

RA

Db 175 LEVIRQELRGFKTKIKVT 192

RESULT 13

Q8IRNO PRELIMINARY; PRT; 249 AA.

AC Q8IRNO;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE CG7090-PB

GN CG10962 OR CG7090.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

SEQUENCE FROM N.A.

RP MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers J.H., Blazey R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,

RA Ballif J.F., Agbayani A., An H.J., Andrews-Frankoch C., Balowin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Buesam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Foaier C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Keichum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,

RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusken D.R., Pacleb J.M.,

RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,

RA Williams S.M., Woodgett J., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.H.O.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster."

RL Science 287:2185-2195(2000).

RN [2]

SEQUENCE FROM N.A.

RP Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,

RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,

RA Banzon J., An H., Baldwin D., Banzon K.Y., Buesam D.A.,

RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,

RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,

RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,

RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,

RA Ibegwam C., Jalali M., Kruse D., Li P., Mattel B., Moshrefi A.,

RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,

RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,

RA Phaulanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,

RA Shaplanenavong S., Svirkas R., Tector C., Tyler D.,

RA Stapleton M., Strong R., Svirkas R., Tector C., Tyler D.,

RA

Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;

RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [3]

SEQUENCE FROM N.A.

RP Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,

RA Hradecky P., Huang Y., Kaminker J.S., Prochink S.E., Smith C.D.,

RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,

Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,

RA Kronmiller B., Marshall B., Milburn G., Richter J., Russo S.,

RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,

RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;

RT "Annotation of Drosophila melanogaster genome."

RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [4]

SEQUENCE FROM N.A.

RP Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter J.C.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

RN [5]

SEQUENCE FROM N.A.

RP FlyBase;

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE003445; AAF6428.1; -

DR FlyBase; FBgn0030073; CG10962.

DR GO; GO:0016491; F:oxidoreductase activity; IEA.

DR GO; GO:0008152; P:metabolism; IEA.

DR InterPro; IPR002198; ADH short.

DR Pfam; PF00106; adh short; 1.

DR PRINTS; PRO0080; SDRFAMILY.

SQ SEQUENCE 249 AA; 27141 MW; 8DAD823CEB7319AF CRC64;

Query Match 28.3%; Score 379; DB 5; Length 249;

Best Local Similarity 35.8%; Pred. No. 8.9e-24;

Matches 92; Conservative 55; Mismatches 88; Indels 22; Gaps 7;

Qy 6 MEMRDRLALVTGSGGIGAAVARALVQOGLKVVGVCARTVGTIEE-----LAAECKSAGYP 61

Db 1 MDRQNEVAVISGASSGIGAACRLVVAAGLVQVGLARRDRLEQLRQSLPAEQRMRFH- 59

Qy 62 GTLLPYRCDLSNEDILSMFSAIRSQHSQVDICINNAGLARPTLLSGSTSGWKMDNFVN 121

Db 60 ----QHKCDVSQELQVDTAFETWIEKELGGIDVLINNAGIVLGGQLIDMPTKDINNILQTN 115

Qy 122 VLALISICTRAYQSKERNVDDGHIININS---MSGHRVLPVLT-HPYSATKYAVTALT 177

Db 116 LMGSIIYCTKLAASSMRRQV-AGHLIFVNSTAGVAGYKPPADSELNAYTFSKFLTAQV 174

Qy 178 EGLRQELREAOHTIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVI 237

Db 175 EICQELINQSKIKTTSINPGWATEIV-----PDETAKLGEV-ILQADDAQAVL 226

Qy 238 YVLSTPAHIQIGDIQMR 254

Db 227 YALSTPPHTQVEQITLR 243

RESULT 14

Q95R56 PRELIMINARY; PRT; 249 AA.

AC Q95R56;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE SD06635P.

GN CG10962 OR CG7090.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

SEQUENCE FROM N.A.

RP Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,

Blank

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2004, 11:04:36 ; Search time 123 Seconds

(without alignments)
597.255 Million cell updates/sec

Title: US-10-063-735-128

Perfect score: 1337

Sequence: 1 MARPGMERWRDLALVTGAS.....STPAHIQIGIQMRPTQVT 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_29Jan04.*

1: geneseqp1980s.*

2: geneseqp1990s.*

3: geneseqp2000s.*

4: geneseqp2001s.*

5: geneseqp2002s.*

6: geneseqp2003as.*

7: geneseqp2003bs.*

8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1337	100.0	260	4	AAU29212	Human PRO
2	1337	100.0	260	4	AB84364	Amino aci
3	1337	100.0	260	4	AB87589	Human PRO
4	1337	100.0	260	5	AB95914	Human sec
5	1337	100.0	260	5	AAU76220	Human 216
6	1337	100.0	260	6	ABU58588	Human PRO
7	1337	100.0	260	6	ABU88136	Novel hum
8	1337	100.0	260	6	ABU84451	Human sec
9	1337	100.0	260	6	ABR66325	Human sec
10	1337	100.0	260	6	ABR65715	Human sec
11	1337	100.0	260	6	ABU99655	Human sec
12	1337	100.0	260	6	ABU82894	Human PRO
13	1337	100.0	260	6	ABU90015	Novel hum
14	1337	100.0	260	6	ABR68264	Human sec
15	1337	100.0	260	6	ABU96317	Novel hum
16	1337	100.0	260	6	ABU92748	Human sec
17	1337	100.0	260	6	ABO08825	Human sec
18	1337	100.0	260	6	ABO02877	Human sec
19	1337	100.0	260	6	ABR75031	Human sec
20	1337	100.0	260	6	ABR94793	Human sec
21	1337	100.0	260	6	ABU85766	Human PRO
22	1337	100.0	260	6	ABU98926	Novel hum
23	1337	100.0	260	6	ABU98141	Novel hum
24	1337	100.0	260	6	ABU91847	Novel hum
25	1337	100.0	260	6	ABU89540	Human PRO

ALIGNMENTS

RESULT 1

AAU29212
ID AAU29212 standard; protein; 260 AA.

XX AC AAU29212;

XX XX

DT 18-DEC-2001 (first entry)

XX DE Human PRO polypeptide sequence #189.

XX KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.

XX OS Homo sapiens.

XX PN WO200168848-A2.

XX XX

PD 20-SEP-2001.

XX PF 28-FEB-2001; 2001WO-US006520.

XX XX

PR 01-MAR-2000; 2000WO-US005601.

PR 02-MAR-2000; 2000WO-US005841.

PR 03-MAR-2000; 2000US-0187202P.

PR 06-MAR-2000; 2000US-0186968P.

PR 14-MAR-2000; 2000US-0189320P.

PR 14-MAR-2000; 2000US-0189328P.

PR 15-MAR-2000; 2000WO-US006884.

PR 21-MAR-2000; 2000US-0190828P.

PR 21-MAR-2000; 2000US-0191007P.

PR 21-MAR-2000; 2000US-0191048P.

PR 21-MAR-2000; 2000US-0191314P.

PR 28-MAR-2000; 2000US-0192655P.

PR 29-MAR-2000; 2000US-0193032P.

PR 29-MAR-2000; 2000US-0193053P.

PR 30-MAR-2000; 2000WO-US008439.

PR 04-APR-2000; 2000US-0194449P.

PR 04-APR-2000; 2000US-0194647P.

PR 11-APR-2000; 2000US-0195975P.

PR 11-APR-2000; 2000US-0196000P.

PR 11-APR-2000; 2000US-0196187P.

PR 11-APR-2000; 2000US-0196690P.

PR 11-APR-2000; 2000US-0196820P.

PR 18-APR-2000; 2000US-0198121P.

PR 18-APR-2000; 2000US-0198585P.

PR 25-APR-2000; 2000US-0199397P.

ABU86381 Human sec
ABU67594 Human sec
ABU80622 Human PRO
ABU90939 Novel hum
ABO33998 Human sec
ABR99540 Human sec
ABR98930 Human sec
ABO16453 Human sec
ABR93353 Human sec
ABO18994 Human sec
ABR78415 Human sec
ABU72015 Novel hum
ABU85151 Novel hum
ABO00290 Novel hum
ABO11622 Human sec
ABO02267 Human sec
ABU88841 Novel hum
ABU83536 Human sec
ABO06337 Novel hum
ABR59373 Human sec

26 1337 100.0 260 6 ABU86381
27 1337 100.0 260 6 ABU67594
28 1337 100.0 260 6 ABU80622
29 1337 100.0 260 6 ABU90939
30 1337 100.0 260 6 ABO33998
31 1337 100.0 260 6 ABR99540
32 1337 100.0 260 6 ABR98930
33 1337 100.0 260 6 ABO16453
34 1337 100.0 260 6 ABR93353
35 1337 100.0 260 6 ABO18994
36 1337 100.0 260 6 ABR78415
37 1337 100.0 260 6 ABU72015
38 1337 100.0 260 6 ABU85151
39 1337 100.0 260 6 ABO00290
40 1337 100.0 260 6 ABO11622
41 1337 100.0 260 6 ABO02267
42 1337 100.0 260 6 ABU88841
43 1337 100.0 260 6 ABU83536
44 1337 100.0 260 6 ABO06337
45 1337 100.0 260 6 ABR59373

PR 25-APR-2000; 2000US-0199550P.
 PR 25-APR-2000; 2000US-0199654P.
 PR 03-MAY-2000; 2000US-0201516P.
 PR 17-MAY-2000; 2000WO-US013705.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 30-MAY-2000; 2000WO-US014941.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 05-JUN-2000; 2000US-0209832P.
 PR 28-JUL-2000; 2000WO-US020710.
 PR 22-AUG-2000; 2000US-00644848.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 08-NOV-2000; 2000WO-US030952.
 PR 01-DEC-2000; 2000WO-US032678.
 PR 20-DEC-2000; 2000WO-US034956.
 PA (GETH) GENENTECH INC.
 XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 FI N-PSDB; AAS46113.
 DR WPI; 2001-602746/68.
 XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the
 PT presence of tumors, such as prostate and breast tumors, in mammals and to
 PT screen for modulators of the compounds.
 XX Claim 11; Fig 378; 774pp; English.
 XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.
 CC The PRO polypeptides and their associated nucleic acids can be used to
 CC detect the presence of a tumour in a mammal by comparing the level of
 CC expression of a PRO polypeptide in a test sample of cells from the animal
 CC and a control sample of normal cells, whereby a higher level of
 CC expression in the test sample indicates the presence of a tumour in the
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats
 CC and rabbits but are preferably human. The polypeptides can be used to
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,
 CC when contacted with it. A specific polypeptide can be used to stimulate
 CC the proliferation or differentiation of chondrocyte cells. The PRO
 CC proteins can be used to determine the presence of tumours and also
 CC susceptibility to tumour development, particularly adrenal, lung, colon,
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids
 CC can be used for genetic analysis of individuals with genetic disorders
 XX Sequence 260 AA;
 SQ
 Query Match 100.0%; Score 1337; DB 4; Length 260;
 Best Local Similarity 100.0%; Pred. No. 1.7e-131;
 Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MARFGMERDRRLALVTGASGGIGAAVARALVQOGLKVVGCAITVGNIEELAAECKSAGY 60
 Db |||||
 QY 61 PGTLLPYRCDSNEEDILSMFSALRSQHSQVDICINNAGLARPDTLGSGTSGWKDMFNV 120
 Db |||||
 QY 61 PGTLLPYRCDSNEEDILSMFSALRSQHSQVDICINNAGLARPDTLGSGTSGWKDMFNV 120
 Db |||||
 QY 121 NVLALSTCTRAYQSMKERNVDDGHIININSMGHRVPLPSVTHFYSAKYAVTALTEGL 180
 Db |||||
 QY 121 NVLALSTCTRAYQSMKERNVDDGHIININSMGHRVPLPSVTHFYSAKYAVTALTEGL 180
 Db |||||
 QY 181 ROELREAOATHRATCISPGVVETQFAKLHDKDPEKAAATYEQMKLKPEDVAEAVIYVL 240
 Db |||||
 QY 181 ROELREAOATHRATCISPGVVETQFAKLHDKDPEKAAATYEQMKLKPEDVAEAVIYVL 240
 Db |||||
 QY 241 STPAHIQIGDIQMRPTEQVT 260
 Db |||||
 QY 241 STPAHIQIGDIQMRPTEQVT 260
 Db |||||

RESULT 2
 AAB84364
 ID AAB84364 standard; protein; 260 AA.
 XX AC AAB84364;
 XX DT 22-AUG-2001 (first entry)
 XX DE Amino acid sequence of human alcohol dehydrogenase 21620.
 XX Human; alcohol dehydrogenase; colon disorder; brain disorder;
 KW skin disorder; heart disorder; blood vessel disorder; kidney disorder;
 KW prostate disorder; skeletal muscle disorder; ovary disorder;
 KW testis disorder; epididymis disorder; spleen disorder; lung disorder;
 KW liver disorder; uterus disorder; endometrium disorder; T-cell disorder;
 KW red cell disorder; thymus disorder; B cell disorder; breast disorder;
 KW thyroid disorder; pancreas disorder; small intestine disorder;
 KW reduced platelet number disorder; precursor T cell neoplasm.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 18..23
 FT /note= "putative N-myristoylation site"
 FT Modified-site 24..29
 FT /note= "putative N-myristoylation site"
 FT Modified-site 40..45
 FT /note= "putative N-myristoylation site"
 FT Modified-site 72..75
 FT /note= "putative casein kinase II phosphorylation site"
 FT Modified-site 89..92
 FT /note= "putative casein kinase II phosphorylation site"
 FT Modified-site 90..95
 FT /note= "putative N-myristoylation site"
 FT Modified-site 109..114
 FT /note= "putative N-myristoylation site"
 FT Modified-site 135..138
 FT /note= "putative casein kinase II phosphorylation site"
 FT Modified-site 135..137
 FT /note= "putative protein kinase C phosphorylation site"
 FT Region 166..176
 FT /note= "short-chain alcohol dehydrogenase family signature"
 FT Modified-site 199..204
 FT /note= "putative N-myristoylation site"
 XX WO200144446-A2.
 XX 21-JUN-2001.
 XX 15-DEC-2000; 2000WO-US033873.
 XX 15-DEC-1999; 99US-00464039.
 XX (MILL-) MILLENNIUM PHARM INC.
 XX Meyers R;
 XX WPI; 2001-390244/41.
 DR N-PSDB; AAB25131.
 XX Novel human alcohol dehydrogenase proteins, 21612, 21615, 21620, 21676,
 FT 33756, useful for treating psoriasis, tropical sprue, pancreatitis,
 FT golter, osteomalacia, endometriosis, angina pectoris, embolism.
 XX Claim 9; Fig 3; 156pp; English.
 CC AAB84364-68 represent human alcohol dehydrogenase proteins, designated
 CC 21620, 33756, 21676, 21612 and 21615, respectively. Alcohol dehydrogenase
 CC polynucleotides and polypeptides are useful for treatment and diagnosis
 CC of disorders mediated by or related to alcohol dehydrogenase. They can be
 CC used for treating disorders of colon, brain, skin, heart, blood vessels,
 CC kidney, prostate, skeletal muscle, ovary, testis and epididymis, spleen,

CC lung, liver, uterus and endometrium, T-cells, red cells, thymus, B cells,
CC breast, thyroid, pancreas, small intestine, reduced platelet number,
CC precursor T cell neoplasms, bone forming cells, and bone marrow cells
XX
SQ Sequence 260 AA;

Query Match 100.0%; Score 1337; DB 4; Length 260;
Best Local Similarity 100.0%; Pred. No. 1.7e-131;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNIEELAAECKSAGY 60
Db 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNIEELAAECKSAGY 60
Qy 61 PGTLPYRCDSLNEEDILSMFSAIRSQHSQVDICINNAGLARPDTLTSGSTSGWKDMFNV 120
Db 61 PGTLPYRCDSLNEEDILSMFSAIRSQHSQVDICINNAGLARPDTLTSGSTSGWKDMFNV 120
Qy 121 NVLALSICTREAYOSMKERNVDDGHIININSMGHRVLPVSVTHFYSAKYAVTALTEGL 180
Db 121 NVLALSICTREAYOSMKERNVDDGHIININSMGHRVLPVSVTHFYSAKYAVTALTEGL 180
Qy 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
Db 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
Qy 241 STPAHIQIGDIQMRPTEQVT 260
Db 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 3

AAB87589
ID AAB87589 standard; protein; 260 AA.
XX
AC AAB87589;
XX
DT 15-MAY-2001 (first entry)
XX
DE Human PRO1774.
XX
KW Human; PRO protein; mapping.
XX
OS Homo sapiens.
XX
PN WO200116318-A2.
XX
PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-US023328.

XX 01-SEP-1999; 99WO-US020111.
PR 15-SEP-1999; 99WO-US021090.
PR 07-DEC-1999; 99US-0169495P.
PR 09-DEC-1999; 99US-0170262P.
PR 11-JAN-2000; 2000US-0175481P.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 01-MAR-2000; 2000US-0187202P.
PR 03-MAR-2000; 2000US-0187202P.
PR 21-MAR-2000; 2000US-0191007P.
PR 30-MAR-2000; 2000WO-US008439.
PR 25-APR-2000; 2000US-0199397P.
PR 22-MAY-2000; 2000WO-US014042.
PR 05-JUN-2000; 2000US-0209832P.

(GETH) GENENTECH INC.

PA Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;
XX Pi Grimaldi CJ, Gurney AL, Watanabe CK, Wood WT;
XX WPI; 2001-183260/18.
DR

DR N-PSDB; AAF92121.
XX
PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular
PT biology, including use as hybridization probes, and in chromosome and
PT gene mapping.
XX

PS Claim 12; Fig 128; 278pp; English.

XX The present sequence is a human PRO polypeptide (secreted and
CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
CC anti-PRO antibodies are useful for preparation of a medicament useful in
CC the treatment of a condition which is responsive to the PRO protein,
CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
CC employed as molecular weight markers for protein electrophoresis. The PRO
CC coding sequence has applications in molecular biology, including use as
CC hybridisation probes, and in chromosome and gene mapping
XX

SQ Sequence 260 AA;

Query Match 100.0%; Score 1337; DB 4; Length 260;
Best Local Similarity 100.0%; Pred. No. 1.7e-131;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNIEELAAECKSAGY 60
Db 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNIEELAAECKSAGY 60
Qy 61 PGTLPYRCDSLNEEDILSMFSAIRSQHSQVDICINNAGLARPDTLTSGSTSGWKDMFNV 120
Db 61 PGTLPYRCDSLNEEDILSMFSAIRSQHSQVDICINNAGLARPDTLTSGSTSGWKDMFNV 120
Qy 121 NVLALSICTREAYOSMKERNVDDGHIININSMGHRVLPVSVTHFYSAKYAVTALTEGL 180
Db 121 NVLALSICTREAYOSMKERNVDDGHIININSMGHRVLPVSVTHFYSAKYAVTALTEGL 180
Qy 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
Db 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
Qy 241 STPAHIQIGDIQMRPTEQVT 260
Db 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 4

ABG95914
ID ABG95914 standard; protein; 260 AA.
XX
AC ABG95914;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human secreted/transmembrane protein PRO1774.
XX
KW Human; secreted protein; transmembrane protein; antirheumatic;
KW antiarthritic; osteopathic; sports-related joint problem;
KW articular cartilage defect; osteoarthritis; rheumatoid arthritis.
XX
OS Homo sapiens.
XX
PN US2002119130-A1.
XX
PD 29-AUG-2002.
XX
PF 06-DEC-2001; 2001US-00006867.

XX 29-OCT-1997; 97US-0063435P.
PR 29-OCT-1997; 97US-0064215P.
PR 22-APR-1998; 98US-0082797P.
PR 29-APR-1998; 98US-0083495P.
PR 15-MAY-1998; 98US-0085579P.
PR 02-JUN-1998; 98US-0087759P.
PR 04-JUN-1998; 98US-0088021P.

Db 181 RQELREAQTHIRATCISPGVVEQAFKLDKQPEKAATYQMKCLKPEDVAEAVIYL 240
QY 241 STPAHIQIGDIQMRTEQVT 260
Db 241 STPAHIQIGDIQMRTEQVT 260
RESULT 5
AAU76220 standard; protein; 260 AA.
XX AAU76220;
XX
XX 08-MAY-2002 (first entry)
XX
XX Human 21620 alcohol dehydrogenase (ADH) protein.
XX
XX Alcohol dehydrogenase; ADH; human; cytostatic; antiinflammatory;
KW cerebroprotective; anti-HIV; immunomodulator; hepatotropic; metastases;
KW pulmonary congestion; Meckel diverticulum; splenic infarction;
KW idiopathic inflammatory bowel disease; jaundice; cholestasis;
KW endometriosis; cerebral oedema; AIDS; leukopaenia; splenomegaly;
KW acquired immune deficiency disease; lupus erythematosus; dermatitis;
KW lung disease; adult respiratory distress syndrome; skin disease;
KW bronchitis; sarcoidosis; pneumothorax; colon disorder; colitis;
KW Crohn's disease; liver disorder; hepatitis; cirrhosis; brain disorder;
KW meningitis; Alzheimer's disease; Huntington's disease; atherosclerosis;
KW ischaemia; chromosome 17 (17q12-21); 21620; enzyme.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Region 166..176
FT /note= "Short chain ADH family signature"
XX
XX US2002010946-A1.
XX
XX 24-JAN-2002.
XX
XX 28-FEB-2001; 2001US-00796089.
XX
XX 15-DEC-1999; 99US-00464039.
XX
XX 15-DEC-2000; 2000WO-US038873.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Meyers R;
XX
XX WPI; 2002-179233/23.
XX
XX N-PSDB; ABK15172.
XX
XX New human alcohol dehydrogenase (ADH) polynucleotides and polypeptides,
XX useful as targets for diagnosing or treating ADH-related or ADH-mediated
XX disorders, e.g. malignant breast metastases, enema or leukopenia.
XX
XX Claim 9; Fig 1A; 80pp; English.
XX
XX This invention relates to the cDNA and protein sequences of 5 novel human
XX alcohol dehydrogenase molecules. The ADH polynucleotides and polypeptides
XX are useful as targets for diagnosing or treating ADH-related or ADH-
XX mediated disorders, e.g. malignant breast, liver, colon or liver
XX metastases, pulmonary congestion or enema, Meckel diverticulum,
XX idiopathic inflammatory bowel disease, jaundice and cholestasis,
XX endometriosis, cerebral oedema, AIDS, or leukopaenia. The sequences may
XX also be used for treating other diseases or disorders such as spleen
XX disorders (splenomegaly, splenic infarction), lung diseases (adult
XX respiratory distress syndrome, bronchitis, sarcoidosis, pneumothorax),
XX colon disorders (colitis, Crohn's disease), liver disorders (hepatitis,
XX cirrhosis), brain disorders (meningitis, Alzheimer's disease,
XX Huntington's disease), heart and blood vessel disorders (atherosclerosis,
XX ischaemia), skin diseases (lupus erythematosus, dermatitis) and many
XX other diseases listed in the specification. The polynucleotides and

CC polypeptides are also useful in screening methods to identify agonists
CC and antagonists for diagnosis or treatment. In particular, the
CC polypeptides and polynucleotides are useful in drug screening assays in
CC cell-based assays or cell-free systems, as well as for biological assays
CC related to ADHs. The ADH polypeptides are also useful for producing
CC antibodies specific for the ADH regions. The polynucleotides and
CC polypeptides may also be used for monitoring therapeutic effects during
CC clinical trials and other treatments. The present sequence represents the
CC human 21620 alcohol dehydrogenase protein of the invention the gene which
XX encodes this protein has been mapped to chromosome 17 (17q12-21)
XX
SQ Sequence 260 AA;
Query Match 100.0%; Score 1337; DB 5; Length 260;
Best Local Similarity 100.0%; Pred. No. 1.7e-131;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARFGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAATVGNIEELAAECKSAGY 60
Db 1 MARFGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAATVGNIEELAAECKSAGY 60
QY 61 PGTILPYRCDLNNEEDILSMFSAIRSOHSGVDICINNAGLARPDLLSGSTSGMKDMFNV 120
Db 61 PGTILPYRCDLNNEEDILSMFSAIRSOHSGVDICINNAGLARPDLLSGSTSGMKDMFNV 120
QY 121 NVLALSICTREAYOSMKERNVDDGHIININSMGHRVPLSVTHFYSAKYAVTALTGL 180
Db 121 NVLALSICTREAYOSMKERNVDDGHIININSMGHRVPLSVTHFYSAKYAVTALTGL 180
QY 181 RQELREAQTHIRATCISPGVVEQAFKLDKQPEKAATYQMKCLKPEDVAEAVIYL 240
Db 181 RQELREAQTHIRATCISPGVVEQAFKLDKQPEKAATYQMKCLKPEDVAEAVIYL 240
QY 241 STPAHIQIGDIQMRTEQVT 260
Db 241 STPAHIQIGDIQMRTEQVT 260
RESULT 6
ABU58588 standard; protein; 260 AA.
XX ID ABU58588 standard; protein; 260 AA.
XX AC ABU58588;
XX
XX 15-APR-2003 (first entry)
XX
XX Human PRO polypeptide #189.
XX
XX Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
KW antibody-dependent enzyme mediated prodrug therapy.
XX
XX Homo sapiens.
XX
XX US2003027272-A1.
XX
XX 06-FEB-2003.
XX
XX 21-JUN-2002; 2002US-00176492.
XX
XX 18-SEP-1997; 97US-0059263P.
XX
XX 18-SEP-1997; 97US-0059266P.
XX
XX 21-OCT-1997; 97US-0062250P.
XX
XX 24-OCT-1997; 97US-0063120P.
XX
XX 24-OCT-1997; 97US-0063121P.
XX
XX 28-OCT-1997; 97US-0063540P.
XX
XX 28-OCT-1997; 97US-0063541P.
XX
XX 28-OCT-1997; 97US-0063544P.
XX
XX 28-OCT-1997; 97US-0063564P.
XX
XX 29-OCT-1997; 97US-0063734P.
XX
XX 31-OCT-1997; 97US-0063870P.
XX
XX 31-OCT-1997; 97US-0064103P.

PR 13-NOV-1997;	97US-0065311P.	PR 17-JUN-1998;	98US-0089538P.
PR 21-NOV-1997;	97US-0066120P.	PR 17-JUN-1998;	98US-0089598P.
PR 24-NOV-1997;	97US-0066466P.	PR 17-JUN-1998;	98US-0089653P.
PR 24-NOV-1997;	97US-0066772P.	PR 18-JUN-1998;	98US-0089908P.
PR 11-DEC-1997;	97US-0069333P.	PR 19-JUN-1998;	98US-0089952P.
PR 12-DEC-1997;	97US-0069425P.	PR 22-JUN-1998;	98US-0090246P.
PR 17-DEC-1997;	97US-0069870P.	PR 22-JUN-1998;	98US-0090252P.
PR 18-DEC-1997;	97US-0068017P.	PR 22-JUN-1998;	98US-0090254P.
PR 10-MAR-1998;	98US-0077450P.	PR 24-JUN-1998;	98US-0090429P.
PR 11-MAR-1998;	98US-0077632P.	PR 24-JUN-1998;	98US-0090435P.
PR 11-MAR-1998;	98US-0077649P.	PR 24-JUN-1998;	98US-0090444P.
PR 20-MAR-1998;	98US-0078886P.	PR 24-JUN-1998;	98US-0090461P.
PR 20-MAR-1998;	98US-0078939P.	PR 24-JUN-1998;	98US-0090535P.
PR 27-MAR-1998;	98US-0079664P.	PR 24-JUN-1998;	98US-0090540P.
PR 27-MAR-1998;	98US-0079786P.	PR 25-JUN-1998;	98US-0090676P.
PR 31-MAR-1998;	98US-0080107P.	PR 25-JUN-1998;	98US-0090678P.
PR 31-MAR-1998;	98US-0080194P.	PR 25-JUN-1998;	98US-0090688P.
PR 01-APR-1998;	98US-0080327P.	PR 25-JUN-1998;	98US-0090690P.
PR 01-APR-1998;	98US-0080333P.	PR 25-JUN-1998;	98US-0090694P.
PR 08-APR-1998;	98US-0081049P.	PR 25-JUN-1998;	98US-0090695P.
PR 08-APR-1998;	98US-0081070P.	PR 25-JUN-1998;	98US-0090696P.
PR 09-APR-1998;	98US-0081195P.	PR 26-JUN-1998;	98US-00105413.
PR 15-APR-1998;	98US-0081838P.	PR 26-JUN-1998;	98US-0090862P.
PR 21-APR-1998;	98US-0082568P.	PR 26-JUN-1998;	98US-0090863P.
PR 21-APR-1998;	98US-0082569P.	PR 26-JUN-1998;	98US-0091010P.
PR 22-APR-1998;	98US-0082704P.	PR 01-JUL-1998;	98US-0091359P.
PR 22-APR-1998;	98US-0082797P.	PR 01-JUL-1998;	98US-0091544P.
PR 28-APR-1998;	98US-0083322P.	PR 02-JUL-1998;	98US-0091478P.
PR 29-APR-1998;	98US-0083496P.	PR 02-JUL-1998;	98US-0091486P.
PR 29-APR-1998;	98US-0083496P.	PR 02-JUL-1998;	98US-0091626P.
PR 29-APR-1998;	98US-0083499P.	PR 02-JUL-1998;	98US-0091628P.
PR 29-APR-1998;	98US-0083559P.	PR 02-JUL-1998;	98US-0091632P.
PR 05-MAY-1998;	98US-0084366P.	PR 24-JUL-1998;	98US-0094006P.
PR 06-MAY-1998;	98US-0084414P.	PR 04-AUG-1998;	98US-0095282P.
PR 07-MAY-1998;	98US-0084639P.	PR 10-AUG-1998;	98US-0095998P.
PR 07-MAY-1998;	98US-0084640P.	PR 10-AUG-1998;	98US-0096012P.
PR 07-MAY-1998;	98US-0084643P.	PR 17-AUG-1998;	98US-0096757P.
PR 15-MAY-1998;	98US-0085579P.	PR 17-AUG-1998;	98US-0096766P.
PR 15-MAY-1998;	98US-0085580P.	PR 17-AUG-1998;	98US-0096867P.
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PR 15-MAY-1998;	98US-0085700P.	PR 17-AUG-1998;	98US-0096897P.
PR 18-MAY-1998;	98US-0086023P.	PR 18-AUG-1998;	98US-0096949P.
PR 22-MAY-1998;	98US-0086392P.	PR 18-AUG-1998;	98US-0096959P.
PR 22-MAY-1998;	98US-0086466P.	PR 18-AUG-1998;	98US-0097022P.
PR 28-MAY-1998;	98US-0087098P.	PR 26-AUG-1998;	98US-0097952P.
PR 28-MAY-1998;	98US-0087208P.	PR 26-AUG-1998;	98US-0097954P.
PR 02-JUN-1998;	98US-0087609P.	PR 26-AUG-1998;	98US-0097955P.
PR 02-JUN-1998;	98US-0087759P.	PR 26-AUG-1998;	98US-0097971P.
PR 03-JUN-1998;	98US-0087827P.	PR 26-AUG-1998;	98US-0097974P.
PR 04-JUN-1998;	98US-0088025P.	PR 26-AUG-1998;	98US-0098014P.
PR 04-JUN-1998;	98US-0088028P.	PR 01-SEP-1998;	98US-0098716P.
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PR 04-JUN-1998;	98US-0088033P.	PR 02-SEP-1998;	98US-0098803P.
PR 04-JUN-1998;	98US-0088326P.	PR 02-SEP-1998;	98US-0098821P.
PR 05-JUN-1998;	98US-0088167P.	PR 02-SEP-1998;	98US-0098843P.
PR 05-JUN-1998;	98US-0088202P.	PR 09-SEP-1998;	98US-0099602P.
PR 05-JUN-1998;	98US-0088212P.	PR 10-SEP-1998;	98US-0099741P.
PR 05-JUN-1998;	98US-0088217P.	PR 10-SEP-1998;	98US-0099754P.
PR 09-JUN-1998;	98US-0088655P.	PR 10-SEP-1998;	98US-0099763P.
PR 10-JUN-1998;	98US-0088722P.	PR 10-SEP-1998;	98US-0099812P.
PR 10-JUN-1998;	98US-0088738P.	PR 15-SEP-1998;	98US-0100388P.
PR 10-JUN-1998;	98US-0088740P.	PR 16-SEP-1998;	98US-0100662P.
PR 10-JUN-1998;	98US-0088811P.	PR 16-SEP-1998;	98US-0100664P.
PR 10-JUN-1998;	98US-0088824P.	PR 16-SEP-1998;	98US-0101751P.
PR 10-JUN-1998;	98US-0088825P.	PR 16-SEP-1998;	98WO-US019330.
PR 10-JUN-1998;	98US-0088826P.	PR 17-SEP-1998;	98US-0100683P.
PR 11-JUN-1998;	98US-0088861P.	PR 17-SEP-1998;	98US-0100684P.
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PR 11-JUN-1998;	98US-0088876P.	PR 17-SEP-1998;	98US-0100930P.
PR 12-JUN-1998;	98US-0089090P.	PR 18-SEP-1998;	98US-0100849P.
PR 12-JUN-1998;	98US-0089105P.	PR 18-SEP-1998;	98US-0101014P.
PR 16-JUN-1998;	98US-0089512P.	PR 18-SEP-1998;	98US-0101069P.
PR 16-JUN-1998;	98US-0089514P.	PR 23-SEP-1998;	98US-0101471P.

PR	23-SEP-1998;	98US-0101472P.	PR	17-OCT-1997;	97US-0062250P.
PR	23-SEP-1998;	98US-0101475P.	PR	21-OCT-1997;	97US-0063486P.
PR	23-SEP-1998;	98US-0101477P.	PR	24-OCT-1997;	97US-0063120P.
PR	24-SEP-1998;	98US-0101738P.	PR	24-OCT-1997;	97US-0063121P.
PR	24-SEP-1998;	98US-0101739P.	PR	28-OCT-1997;	97US-0063540P.
PR	24-SEP-1998;	98US-0101743P.	PR	28-OCT-1997;	97US-0063541P.
PR	24-SEP-1998;	98US-0101922P.	PR	28-OCT-1997;	97US-0063544P.
PR	25-SEP-1998;	98US-0101786P.	PR	28-OCT-1997;	97US-0063564P.
PR	29-SEP-1998;	98US-0102207P.	PR	29-OCT-1997;	97US-0063734P.
PR	29-SEP-1998;	98US-0102240P.	PR	31-OCT-1997;	97US-0063870P.
PR	29-SEP-1998;	98US-0102330P.	PR	31-OCT-1997;	97US-0064103P.
PR	29-SEP-1998;	98US-0102331P.	PR	13-NOV-1997;	97US-0065311P.
PR	30-SEP-1998;	98US-0102487P.	PR	21-NOV-1997;	97US-0066120P.
PR	30-SEP-1998;	98US-0102570P.	PR	24-NOV-1997;	97US-0066456P.
PR	30-SEP-1998;	98US-0102571P.	PR	11-DEC-1997;	97US-0066772P.
PR	01-OCT-1998;	98US-0102684P.	PR	12-DEC-1997;	97US-0069335P.
PR	01-OCT-1998;	98US-0102687P.	PR	17-DEC-1997;	97US-0069425P.
PR	02-OCT-1998;	98US-0102965P.	PR	18-DEC-1997;	97US-0069870P.
PR	06-OCT-1998;	98US-0103258P.	PR	10-MAR-1998;	97US-0068017P.
PR	06-OCT-1998;	98US-0103449P.	PR	11-MAR-1998;	98US-0077450P.
PR	07-OCT-1998;	98US-0016897B.	PR	11-MAR-1998;	98US-0077632P.
Query Match 100.0%; Score 1337; DB 6; Length 260;					98US-0077649P.
Best Local Similarity 100.0%; Pred. No. 1.7e-131;					98US-0078886P.
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					98US-0078939P.
Qy	1	MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCA	PR	27-MAR-1998;	98US-0079664P.
Db	1	MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCA	PR	27-MAR-1998;	98US-0079786P.
Qy	61	PGTLIPYRCDLSNEEDILSMFSAIRSQHSQGVDCINNAGLAR	PR	31-MAR-1998;	98US-0080107P.
Db	61	PGTLIPYRCDLSNEEDILSMFSAIRSQHSQGVDCINNAGLAR	PR	31-MAR-1998;	98US-0080194P.
Qy	121	NVLALSICTREAYQSMKERNVDDGHIININSMGHRVPLSV	PR	01-APR-1998;	98US-0080327P.
Db	121	NVLALSICTREAYQSMKERNVDDGHIININSMGHRVPLSV	PR	01-APR-1998;	98US-0080333P.
Qy	181	ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAA	PR	08-APR-1998;	98US-0081049P.
Db	181	ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAA	PR	08-APR-1998;	98US-0081070P.
Qy	241	STPAHIQIGDIQMRPTEQVT 260	PR	09-APR-1998;	98US-0081195P.
Db	241	STPAHIQIGDIQMRPTEQVT 260	PR	15-APR-1998;	98US-0081838P.
RESULT 7					98US-0082568P.
ID	ABU88136		PR	21-APR-1998;	98US-0082569P.
XX	ABU88136 standard; protein; 260 AA.		PR	22-APR-1998;	98US-0082704P.
AC	ABU88136;		PR	22-APR-1998;	98US-0082797P.
XX	07-JUL-2003 (first entry)		PR	28-APR-1998;	98US-0083322P.
DT	Novel human secreted and transmembrane protein	PRO1774.	PR	28-APR-1998;	98US-0083496P.
DE	Human; secreted and transmembrane protein: PRO;	gene therapy;	PR	29-APR-1998;	98US-0083499P.
XX	tumour necrosis factor-alpha release; TNF-alpha	release;	PR	29-APR-1998;	98US-0083559P.
KW	chondrocyte proliferation; chondrocyte differentia	tion; tumour;	PR	05-MAY-1998;	98US-0084366P.
KW	adrenal tumour; lung tumour; colon tumour; breast	tumour;	PR	06-MAY-1998;	98US-0084414P.
KW	prostate tumour; rectal tumour; cervical tumour;	liver tumour.	PR	07-MAY-1998;	98US-0084639P.
XX	Homo sapiens.		PR	07-MAY-1998;	98US-0084640P.
OS			PR	15-MAY-1998;	98US-0085579P.
XX	US2003032127-A1.		PR	15-MAY-1998;	98US-0085580P.
XX	13-FEB-2003.		PR	15-MAY-1998;	98US-0085582P.
XX	26-JUN-2002; 2002US-00183012.		PR	18-MAY-1998;	98US-0086023P.
XX	18-SEP-1997; 97US-0059263P.		PR	22-MAY-1998;	98US-0086392P.
PR	18-SEP-1997; 97US-0059266P.		PR	22-MAY-1998;	98US-0086486P.
PR			PR	28-MAY-1998;	98US-0087098P.
PR			PR	28-MAY-1998;	98US-0087208P.
PR			PR	02-JUN-1998;	98US-0087609P.
PR			PR	02-JUN-1998;	98US-0087759P.
PR			PR	03-JUN-1998;	98US-0087827P.
PR			PR	04-JUN-1998;	98US-0088025P.
PR			PR	04-JUN-1998;	98US-0088028P.
PR			PR	04-JUN-1998;	98US-0088029P.
PR			PR	04-JUN-1998;	98US-0088033P.
PR			PR	04-JUN-1998;	98US-0088326P.
PR			PR	05-JUN-1998;	98US-0088167P.
PR			PR	05-JUN-1998;	98US-0088202P.
PR			PR	05-JUN-1998;	98US-0088212P.
PR			PR	05-JUN-1998;	98US-0088217P.
PR			PR	09-JUN-1998;	98US-0088655P.
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[illegible]

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PR	15-SEP-1998;	98US-0100388P.	KW	bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
PR	16-SEP-1998;	98US-0100662P.	KW	adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
PR	16-SEP-1998;	98US-0100664P.	KW	liver; drug screening; transgenic animal; genetic analysis;
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PR	02-OCT-1998;	98US-0102965P.	XX	
PR	06-OCT-1998;	98US-0103258P.	XX	
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Db	1	MARQMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAVTGNTIEELAAECKSAGY 60		
Qy	61	PGTLIPYRCDLSNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLISGSTSGWKDMFNV 120		
Db	61	PGTLIPYRCDLSNEEDILSMFSAIRSQHSGVDICINNAGLARPDTLISGSTSGWKDMFNV 120		
Qy	121	NVLALSICTRAYOSMKERNVDDGHIININSMGHRVPLSVTHFYATKYAVTALTEGL 180		
Db	121	NVLALSICTRAYOSMKERNVDDGHIININSMGHRVPLSVTHFYATKYAVTALTEGL 180		
Qy	181	RQELREACTHRAICISPGVWETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240		
Db	181	RQELREACTHRAICISPGVWETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240		
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AC ABR66325;				
XX				
DT 05-AUG-2003 (first entry)				
XX				

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PR	02-JUN-1998;	98US-0087759P.	PR	26-AUG-1998;	98US-0097971P.
PR	03-JUN-1998;	98US-0087827P.	PR	26-AUG-1998;	98US-0097974P.
PR	04-JUN-1998;	98US-0088025P.	PR	01-SEP-1998;	98US-0098014P.
PR	04-JUN-1998;	98US-0088028P.	PR	01-SEP-1998;	98US-0098723P.
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PR	05-JUN-1998;	98US-0088167P.	PR	02-SEP-1998;	98US-0098843P.
PR	05-JUN-1998;	98US-0088202P.	PR	09-SEP-1998;	98US-0099602P.
PR	05-JUN-1998;	98US-0088212P.	PR	10-SEP-1998;	98US-0099741P.
PR	05-JUN-1998;	98US-0088217P.	PR	10-SEP-1998;	98US-0099754P.
PR	10-JUN-1998;	98US-0088655P.	PR	10-SEP-1998;	98US-0099763P.
PR	10-JUN-1998;	98US-0088722P.	PR	10-SEP-1998;	98US-0099812P.
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PR	11-JUN-1998;	98US-0088861P.	PR	17-SEP-1998;	98US-0100683P.
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PR	12-JUN-1998;	98US-0089090P.	PR	17-SEP-1998;	98US-0100930P.
PR	12-JUN-1998;	98US-0089105P.	PR	18-SEP-1998;	98US-0100849P.
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PR	24-JUN-1998;	98US-0090461P.	PR	29-SEP-1998;	98US-0102240P.
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PR	25-JUN-1998;	98US-0090678P.	PR	30-SEP-1998;	98US-0102570P.
PR	25-JUN-1998;	98US-0090688P.	PR	30-SEP-1998;	98US-0102571P.
PR	25-JUN-1998;	98US-0090690P.	PR	01-OCT-1998;	98US-0102684P.
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PR	26-JUN-1998;	98US-00105413.			
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PR	26-JUN-1998;	98US-0091010P.			
PR	01-JUL-1998;	98US-0091			

RESULT 10
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ID ABR65715 standard; protein; 260 AA.
XX
AC ABR65715;
XX
DT 05-AUG-2003 (first entry)
XX
DE Human secreted polypeptide PRO1774, SEQ ID NO:378.
XX
KW Human; PRO; secreted protein; transmembrane protein;
extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
chondrocyte; proliferation; differentiation; cartilage disorder;
bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
liver; drug screening; transgenic animal; genetic analysis;
antiarthritic; vulnery; gene therapy.
XX
OS Homo sapiens.
XX
FN US2003036159-A1.
XX
PD 20-FEB-2003.
XX
PF 02-JUL-2002; 2002US-00188773.
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PR	29-SEP-1998;	98US-0102331P.	
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PR	30-SEP-1998;	98US-0102570P.	
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Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Db	1	MARFGMRWRDLALVTGASGIGAAVARALVQGLKVGCAVTGNIIEELAAECKAGY	60
Qy	61	PGTLIPYRCDLSNEEDILSMFSAIRSOHSGVDICINNAGLARPTLLSGSTSGWKDMFNV	120
Db	61	PGTLIPYRCDLSNEEDILSMFSAIRSOHSGVDICINNAGLARPTLLSGSTSGWKDMFNV	120
Qy	121	NVLALSICTREAYQSMKERNVDDGHHININSMGSHRVLPLSVTHFYSAKYAVTALTEGL	180
Db	121	NVLALSICTREAYQSMKERNVDDGHHININSMGSHRVLPLSVTHFYSAKYAVTALTEGL	180

Qy	181	ROELREAQTHIRATCISPGVWETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL	240
Db	181	ROELREAQTHIRATCISPGVWETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL	240
Qy	241	STPAHIQIGDIQMRPTEQVT	260
Db	241	STPAHIQIGDIQMRPTEQVT	260
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ABU99655			
ID	ABU99655	standard; protein; 260 AA.	
XX	AC	ABU99655;	
XX	DT	09-AUG-2003 (first entry)	
XX	DE	Human secreted/transmembrane protein (PRO) #189.	
XX	KW	Human; secreted and transmembrane protein; PRO; TNF-alpha;	
KW	KW	tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;	
XX	OS	tissue typing.	
XX	XX	Homo sapiens.	
PN	US2003040070-A1.		
PD	27-FEB-2003.		
XX	XX	27-JUN-2002; 2002US-00184627.	
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PR	18-SEP-1997;	97US-0059266P.	
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PR	21-OCT-1997;	97US-0063486P.	
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PR	31-OCT-1997;	97US-0063870P.	
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PR	21-NOV-1997;	97US-0066120P.	
PR	24-NOV-1997;	97US-0066466P.	
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PR	11-DEC-1997;	97US-0069335P.	
PR	12-DEC-1997;	97US-0069425P.	
PR	17-DEC-1997;	97US-0069870P.	
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PR	10-MAR-1998;	98US-0077450P.	
PR	11-MAR-1998;	98US-0077632P.	
PR	11-MAR-1998;	98US-0077649P.	
PR	20-MAR-1998;	98US-0078886P.	
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PR	31-MAR-1998;	98US-0080107P.	
PR	31-MAR-1998;	98US-0080194P.	
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PR	01-APR-1998;	98US-0080333P.	
PR	08-APR-1998;	98US-0081049P.	
PR	08-APR-1998;	98US-0081070P.	
PR	09-APR-1998;	98US-0081195P.	
PR	15-APR-1998;	98US-0081838P.	
PR	21-APR-1998;	98US-0082568P.	
PR	21-APR-1998;	98US-0082569P.	
PR	22-APR-1998;	98US-0082704P.	
PR	22-APR-1998;	98US-0082797P.	
PR	28-APR-1998;	98US-0083322P.	

Dd	1	MARPQMERWRDLALVTGAGSGIGAAVARALVQQGLKVVGCARTVGNIEELAAECKSAGY	60	PR	08-APR-1998;	98US-0081070P.
Qy	61	PGTLIPYRCDLSNEEDIILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV	120	PR	09-APR-1998;	98US-00811195P.
Dd	61	PGTLIPYRCDLSNEEDIILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMFNV	120	PR	15-APR-1998;	98US-0081838P.
Qy	121	NVLALSICTREAYQSMKERNVDDGHIININSMGHRVLPVLSVTHFYPSATKYAVTALTEGL	180	PR	21-APR-1998;	98US-0082568P.
Dd	121	NVLALSICTREAYQSMKERNVDDGHIININSMGHRVLPVLSVTHFYPSATKYAVTALTEGL	180	PR	21-APR-1998;	98US-0082569P.
Qy	181	ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL	240	PR	22-APR-1998;	98US-0082704P.
Dd	181	ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL	240	PR	22-APR-1998;	98US-0082797P.
Qy	241	STPAHIQIGDIQMRPTEQVT	260	PR	28-APR-1998;	98US-0083322P.
Dd	241	STPAHIQIGDIQMRPTEQVT	260	PR	28-APR-1998;	98US-0083322P.
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XX	AC	AC				98US-0084366P.
DT	27-JUN-2003	(first entry)				98US-0084414P.
DE	Human PRO polypeptide #189.					98US-0084639P.
XX	Human; PRO polypeptide; secreted and transmembrane protein; tumour;					98US-0084643P.
KW	chromosome mapping; gene mapping; cytostatic.					98US-0085579P.
KW						98US-0085580P.
OS	Homo sapiens.					98US-0085582P.
XX	US2003032113-Al.					98US-0085700P.
XX	13-FEB-2003.					98US-0086023P.
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PR	29-OCT-1997; 97US-0063734P.					98US-0088033P.
PR	31-OCT-1997; 97US-0063870P.					98US-0088167P.
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PR	12-DEC-1997; 97US-0069335P.					98US-0088811P.
PR	17-DEC-1997; 97US-0069425P.					98US-0088824P.
PR	18-DEC-1997; 97US-0069870P.					98US-0088825P.
PR	10-MAR-1998; 98US-0077450P.					98US-0088861P.
PR	11-MAR-1998; 98US-0077632P.					98US-0088863P.
PR	11-MAR-1998; 98US-0077649P.					98US-0088876P.
PR	20-MAR-1998; 98US-0078886P.					98US-0089090P.
PR	20-MAR-1998; 98US-0078939P.					98US-0089105P.
PR	27-MAR-1998; 98US-0079664P.					98US-0089512P.
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PR	01-APR-1998; 98US-0080194P.					98US-0089598P.
PR	01-APR-1998; 98US-0080327P.					98US-0089653P.
PR	01-APR-1998; 98US-0080333P.					98US-0089908P.
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PR 26-JUN-1998; 98US-0090862P.
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PR 06-OCT-1998; 98US-0103449P.

PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98US-0103395P.

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Best Local Similarity 100.0%; Pred. No. 1.7e-131;
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DB 1 MARPGMERWRDLALVTGASGGIGAAVARALVQOGLKVVGCAARTVGNIEELAAECKSAGY 60
QY 61 PGTLLPYRCDLNNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMENV 120
DB 61 PGTLLPYRCDLNNEEDILSMFSAIRSQHSQVDICINNAGLARPDPTLLSGSTSGWKDMENV 120
QY 121 NVLALSICTREAYOSMKERNVDDGHIININSMGHRVPLSVTHFYFSATKYAVTALTGL 180
DB 121 NVLALSICTREAYOSMKERNVDDGHIININSMGHRVPLSVTHFYFSATKYAVTALTGL 180
QY 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
DB 181 ROELREAQTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQMKCLKPEDVAEAVIYVL 240
QY 241 STPAHIQIGDIQMRPTEQVT 260
DB 241 STPAHIQIGDIQMRPTEQVT 260

RESULT 13
ABU90015
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AC ABU90015;
XX
DT 11-AUG-2003 (first entry)
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XX
DE Novel human secreted and transmembrane protein PRO1774.
XX
KW Human; gene therapy; tissue typing; tumour; chondrocyte proliferation;
KW chondrocyte differentiation; tumour necrosis factor-alpha release;
XX affinity purification.
OS Homo sapiens.
XX
XX US2003036147-A1.
XX
XX 20-FEB-2003.
XX
XX 02-JUL-2002; 2002US-00187741.
XX
PR 18-SEP-1997; 97US-0059263P.
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PR 17-OCT-1997; 97US-0062250P.
PR 21-OCT-1997; 97US-0063486P.
PR 24-OCT-1997; 97US-0063120P.
PR 24-OCT-1997; 97US-0063121P.
PR 28-OCT-1997; 97US-0063540P.
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PR 17-SEP-1998;	98US-0100684P.
PR 17-SEP-1998;	98US-0100919P.
PR 17-SEP-1998;	98US-0100930P.
PR 18-SEP-1998;	98US-0100849P.
PR 18-SEP-1998;	98US-0101014P.
PR 18-SEP-1998;	98US-0101068P.
PR 23-SEP-1998;	98US-0101471P.
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PR 23-SEP-1998;	98US-0101477P.
PR 24-SEP-1998;	98US-0101738P.
PR 24-SEP-1998;	98US-0101739P.
PR 24-SEP-1998;	98US-0101743P.
PR 24-SEP-1998;	98US-0101922P.
PR 25-SEP-1998;	98US-0101786P.
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GenCore version 5.1.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 16, 2004, 14:46:16 ; Search time 3081 Seconds
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Searched: 3470272 seqs, 21671516995 residues

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Listing first 45 summaries

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26	406.5	30.4	168583	3	AC104510	Drosophil
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ALIGNMENTS

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VERSION      BC002731.2 GI:33877092
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SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
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AUTHORS      Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
      Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
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      Schnerfeld,A., Schein,J.E., Jones,S.J. and Marra,M.A.
      Generation and initial analysis of more than 15,000 full-length
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JOURNAL      Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
MEDLINE      22388257
PUBMED      12477932
2 (bases 1 to 1501)
Strausberg,R.
Direct Submission
Submitted (05-FEB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:12803782.
Contact: MGC help desk
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@hgrl.nih.gov
Akhrer,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
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 Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and
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Qy	181	ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal	200
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Qy	201	ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThr	220
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Qy	221	TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu	240
Db	772	TATGAGCAAAAGAGTGCTCAAAACCCGAGGATGGCCGAGCTGTATCTACGTCTCTC	831
Qy	241	SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr	260
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RESULT 4			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			

JOURNAL	Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA		
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Qy	41	CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyr	60
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Qy	61	ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet	80
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Qy	81	PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu	100
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Qy	121	AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn	140
Db	472	AACGTGCTGGGCCCTCAGCATCTGCACACGGGAAAGCTTACCAGTCCATGAAGAGCGGAAT	531
Qy	141	ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu	160
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Db	592	TCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGTCTGACAGAGGAGCTG	651
Qy	181	ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal	200
Db	652	AGGCAAGAGCTTCGGGAGGCCAGACCCACATCCGAGCCACGTGCTCTCCAGGTGTG	711

Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA

Location/Qualifiers
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Qy 21 GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValGly 40
Db 172 GGGGCAATCGCGCGCGCGTGGCGCGGCCCTGGTCCAGCAGGAGCTGAAGTGTGGGC 231
Qy 41 CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
Db 232 TGCGCCGCGCATGTGGGCAACATCGAGGAGCTGGCTGCTGAATGTAAGATGCAGGCTAC 291
Qy 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet 80
Db 292 CCCGGGACTTTGATCCCTACAGATGTGACCTATCAAAATGAAGAGGACATCTCTCCATG 351
Qy 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu 100
Db 352 TTCTCAGTATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACAATGCTGGCTG 411
Qy 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnVal 120
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Qy 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
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Qy 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
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Qy 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
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Qy 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
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QY 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
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QY 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
Db 832 AGCACCCCGCACATCCAGATTGGAGACATCCAGATGAGGCCACGAGGAGGAGTGC 891

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LOCUS AXI79289 1909 bp DNA linear PAT 03-JUL-2001
DEFINITION Sequence 2 from Patent WO0144446.
ACCESSION AXI79289
VERSION AXI79289.1 GI:14598959
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Meyers, R.
TITLE 21612, 21615, 21620, 21676, 33756, novel human alcohol
JOURNAL dehydrogenases
PUBLISHED 21-JUN-2001
MILENMIUM Pharmaceuticals, Inc. (US)
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QY 41 CysAlaArgThrValGlyAsnIleGluGluLeuAlaGluCysLysSerAlaGlyTyr 60
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QY 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet 80
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LOCUS AXI768992 2077 bp DNA linear PAT 02-JUL-2003
DEFINITION Sequence 109 from Patent WO02098917.
ACCESSION AXI768992
KEYWORDS AXI768992.1 GI:32437160
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Guo, X., Fernandes, E., Li, L., Kekuda, R., Liu, Y., Leite, M.,
Spytek, K.A., Ji, W., Casman, S.J., Boldog, F.L., Patturajan, M.,
Vernet, C.A., Ballinger, R.A., Malyankar, U.M., Tchernev, V.T.,
Blalock, A.D., Gusev, V.Y., Rastelli, L., Mezes, P.D., Ellerman, K.,
Heyes, M., Herrmann, J.L., Shinkets, R.A., Ioime, N., Pena, C.E.,
Shenoy, S.G., Taupier, R.J., Gerlach, V. and Gorman, L.
TITLE Human proteins and nucleic acids encoding same
JOURNAL Patent: WO 02098917-A 109 12-DEC-2002;
Curagen Corporation (US)
FEATURES
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		ORGANISM	Mus musculus
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		AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.D., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Young, A.C., Shevchenko, Y., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Green, E.D., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
		TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
		JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
		MEDLINE	22388257
		PUBMED	12477932
		REFERENCE	2 (bases 1 to 1398)
		AUTHORS	Strausberg, R.
		TITLE	Direct Submission
		JOURNAL	Submitted (01-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
		REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
		COMMENT	Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcdpaxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.
		FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Series: IRAC Plate: 25 Row: b Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: Genomescan gene prediction, Similarity but not identity to protein. Location/Qualifiers 1..1398 /organism="Mus musculus" /mol_type="mRNA" /strain="FVB/N" /db_xref="taxon:10090" /clone="MGC:18716 IMAGE:4219994" /tissue_type="Colon, normal. 5 month old male mouse." /clone_lib="NCI CGAP_Co24" /lab_host="DH105" /note="Vector: pCMV-SPORT6" 1..1398 /gene="BC022224" /note="synonym: MGC18716" /db_xref="LocusID:192570" /db_xref="MGI:2652816" 305..850 /codon_start=1
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		VERSION	BC022224.1 GI:18490589
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Query Match: 94.02% Indels: 0
DB: 10 Gaps: 0
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Db 128 GGGGGCATCGGTGGCGCGGTGGCGCGGCATAGTCCAGCAGGAGCTGAAGGTTGTGGGT 187
QY 41 CysAlaArgThrValGlyAsnIleGluGluLeuAlaGluCysLysSerAlaGlyTyr 60
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QY 161 SerValThrHisPheTyrSerAlaThrIlystYrAlaValThrAlaLeuThrGluGlyLeu 180
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QY 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
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QY 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaThr 220
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QY 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
Db 728 TATGACACATAAAGTGTCTCAGACACGAGGACGTGCTGAGGCTGTCTACGTCTTCTT 787
QY 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260

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Db 788 AGCACACCCCAATGTTTCAGGTTGGTGACATCCAGATGAGGCCACACAGAGGTTGACC 847
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RESULT 8
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LOCUS Homo sapiens cDNA: FLJ22543 fis, clone HSI00212.
DEFINITION AK026196
ACCESSION AK026196.1 GI:10438967
VERSION oligo capping; fis (full insert sequence).
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1
Watanabe, K., Kumagai, A., Itakura, S., Yamazaki, M., Tashiro, H.,
Ota, T., Suzuki, Y., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T.,
Nakamura, Y., Isogai, T. and Sugano, S.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 1410)
Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T.,
Shibahara, T., Tanaka, T. and Nakamura, Y.
Direct Submission
Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure Analysis, Human
Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Japan (E-mail: flicdn@ims.u-tokyo.ac.jp, Tel: 81-3-5449-5286,
Fax: 81-3-5449-5416)
NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing; Research Association for Biotechnology; cDNA library
construction, 5'- & 3'-end one pass sequencing; Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="HSI00212"
/tissue_type="human small intestine"
/clone_lib="HSI"
/notes="cloning vector pME18SFL3"
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Alignment Scores:
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Query Match: 82.65% Indels: 4
DB: 9 Gaps: 2
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QY 20 SerGlyGlyIle-----GlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLys 37
Db 51 TCTGGTGGGTCTAGGCGCGGATCCCAAGCAGGAGTCCGCGCGCGGCGGAGAGCGG 110
QY 38 -----ValValGlyCysAlaArgThrValGlyAsnIleGluGluLeuAlaGluCys 55
Db 111 CCGGGGCTGAGCTCTCGACCCCGCTGTCGGGCAACATCGAGGAGCTGGCTGTAATGT 170

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Qy 56 LysSerAlaGlyTyrProGlyThrIleuLeuProTyrArgCysAspLeuSerAsnGluGlu 75
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Qy 76 AspIleLeuSerMetPheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIle 95
Db 231 GACATCTCTCCATGCTCTAGCTATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATC 290
Qy 96 AsnAsnAlaGlyLeuAlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpLys 115
Db 291 AACAAATGCTGGCTTGGCCCGCTGACACCTGCTCTCAGGACGACCAAGTGGTGAAG 350
Qy 116 AspMetPheAsnValAsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSer 135
Db 351 GACATGTTCAATGTGAACGTGCTGGCCCTCAGCATCTGCACACCGGAAGCCTACAGTCC 410
Qy 136 MetLysGluArgAsnValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHis 155
Db 411 ATGAAGAGCGGAATGTGACGATGGGCACATCATTAACATCAATAGCATGTCTGGCCAC 470
Qy 156 ArgValLeuProLeuSerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAla 175
Db 471 CGAGTGTACCCCTCTCTGTGACCCACTTCTATAGTGCACCAAGTATGCCGTCACTGCG 530
Qy 176 LeuThrGluGlyLeuArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCys 195
Db 531 CTGACAGAGGAGTACGAGCAAGAGTCTCGGAGGCCACAGCCACATCCGAGCCACGTGC 590
Qy 196 IleSerProGlyValValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGlu 215
Db 591 ATCTCTCAGGTGTGGTGGAGACACATTCGGCTTCAAACTCCACGACAGGACCTGAG 650
Qy 216 LysAlaAlaAlaThrTyrGluGlnMetLysCysLysLeuLysProGluAspValAlaGluAla 235
Db 651 AAGGAGAGTGCACCATATGAGCAAAATGAAGTGTCTCAAAACCGAGGATGTGGCCGAGCT 710
Qy 236 VallIleTyrValLeuSerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgPro 255
Db 711 GTTATCTACGTCTCAGACACCCCGCACACATCCAGATTGGAGATCCAGATGAGGCC 770
Qy 256 ThrGluGlnValThr 260
Db 771 ACGGAGCAGGTGACC 785

RESULT 9
AC017377
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1715 bp mRNA linear INV 30-NOV-2002
Ciona intestinalis cDNA, clone:citb005002, full insert sequence.
AK116054
AK116054.1 GI:23588453
FLI_CDNA.
Ciona intestinalis
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cionidae; Ciona.
Satou,Y., Yamada,L., Mochizuki,Y., Takatori,N., Kawashima,T.,
Sasaki,A., Hanaguchi,M., Awazu,S., Yagi,K., Sasaki,Y.,
Nakayama,A., Ishikawa,H., Inaba,K. and Satoh,N.
A cDNA resource from the basal chordate Ciona intestinalis
Genes 33 (4), 153-154 (2002)
22191024
12203911
2 (bases 1 to 1715)
Satou,Y. and Satoh,N.
Direct Submission
Submitted (04-OCT-2002) Nori Satoh, Kyoto University, Department of
Zoology; Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
(E-mail:saton@scs.kyoto-u.ac.jp, Tel:81-75-753-4095,
Fax:81-75-705-1113)
Ciona intestinalis cDNA Project (URL:
http://ghost.zool.kyoto-u.ac.jp/indexr1.html).

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FEATURES

source

Location/Qualifiers

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Best Local Similarity: 47.83% Mismatches: 76
Query Match: 47.64% Indels: 4
Gaps: 2

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US-10-063-735-128 (1-260) x AK116054 (1-1715)

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Db 12 ATGGATAGGTGGATAGTAAGTTGCTATCTCTACCTGGAGGCTATGAAGGCATTGGTGA 71
Qy 26 AlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGlyCysAlaArgThrVal 45
Db 72 GCAACTGTAAAGTGGTTCAGTCATGGAATGAAAGTGGTTGGTTGTCAAGAAATGAG 131
Qy 46 GlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyrProGlyThrIleuLe 65
Db 132 GAAAACTGAAACAAATTCGCATCGGAATCAACCGGAAGGGT--CAAGGGGAGATGTT 188
Qy 66 ProTyrArgCysAspLeuSerAsnGluAlaAspIleLeuSerMetPheSerAlaIleArg 85
Db 189 CTTTCAAAATGTGATGTCAGATGAATCCACATCTTAGAAATGTTAAATTTGTGAAG 248
Qy 86 SerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeuAlaArgProAspThr 105
Db 249 GAGAAAGTTTGGAGCAGTACATCTGTGTTAATAATGCTGGGATAGCATTTGATTCTCA 308
Qy 106 LeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnValAsnValLeuAlaLeu 125
Db 309 ATATCATCGGAGACTCACAGAAATGGAAGAGAAATCTTGGACACCAATGTTCTTGGTCT 368
Qy 126 SerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsnValAspAspGlyHis 145
Db 369 AGCATCTGTTCCCGTGAAGCAGTACAACTAATGAAGAGACTGGAGTCGACGATGGCAT 428
Qy 146 IleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeuSerValThrHisPhe 165
Db 429 ATAGTTAATATCAATAGTGTGCTGCTCAGAGGGTGGTGGACAAAGCCAAATG----- 479
Qy 166 TyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeuArgGlnGluLeuArg 185
Db 480 TATGCTGCATCTAAGTTTGCAGTCACTGCTCTTACTGAAGGTCTAAGAAAGAGAGTTGCT 539
Qy 186 GluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyValValGluThrGlnPhe 205
Db 540 TCTGCAATACTCATATTTCGTACAACTTCAATTTCCACGAGGCTATGTCAAAACGGAAT 599
Qy 206 AlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThrTyrGluGlnMetLys 225
Db 600 TTTCACAAAATTTACCACGACACTGAATGCGTCGAAATAATCTCTGAAATCTCTTAAA 659
Qy 226 CysLeuLysProGluAspValAlaGluAlaValIleTyrValLeuSerThrProAlaHis 245
Db 660 TGCCTTGAAGGTGAAGATATTGCTGCTGTGCTGTATGTCAGTGTCCGACCTCTCAT 719
Qy 246 IleGlnIleGlyAspIleGlnMetArgProThrGluGln 258
Db 720 GTTGATATTAAATGAGATTATCATACGACCTGTGTGACCA 758

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RESULT 10

AC017377

LOCUS

140468 bp

DNA

linear

HTG 09-DEC-1999

Qy	177	ThrGluGlyLeuArgGlnGlnLeuArgGluAlaGlnThrHisIleArgAlaThrCysIle	196
Db	33130	ACAGAGACATATCGGCAGGAATTTTCAGCTGCATCGACCAAAATCGGGTTACTGCATC	33188
Qy	197	SerProGlyValValGluThrGlnPheAlaPheLeuHisAspLysAspProGluLys	216
Db	33190	TGTCCTGTGTCGGTGAACACGACATCTTC-----CCGGAAGAG	33228
Qy	217	AlaAlaAlaThrTyrrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaVal	236
Db	33229	ATCCATTTTACGTCAAGACATCGGCACACTCGAACCGAACCATTCGGACGCGATG	33288
Qy	237	IleTyrrValLeuSerThrProAlaHisIleGlnIleGlyAspIle	251
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DEFINITION	Drosophila melanogaster DNA sequence (pls DS06106 (D123), DS05973 (D122), and DS08584 (D118)), complete sequence.		
ACCESSION	AC004758 AC004418 AC003710 AC002609 AC002610 AC002611 AC002612 AC002613 AC002614 AC002615 AC002616 AC002617 AC002618 AC003132 AC002619 AC004270 AC001713 AC001714 AC001715 AC001716 AC002591 AC003177 AC002592 AC002593 AC002594 AC002595 AC002596 AC001718 AC001719 AC002597 AC002598 AC002599 AC001720 AC001721 AC002600 AC001722 AC002601 AC001723 AC001724 AC002602 AC0032603 AC001725 AC001726 AC002604 AC002605 AC002606 AC002607 AC0032608 AC001727 AC004758 AC002583 AC003706 AC002584 AC002585 AC003707 AC003708		
VERSION	AC004758.1	GI:3168618	
KEYWORDS	HTG.		
SOURCE	Drosophila melanogaster (fruit fly)		
ORGANISM	Drosophila melanogaster		
REFERENCE	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.		
AUTHORS	Celisner,S.E., Aghavani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Chew,M., Doyle,C.M., Farfan,D.E., Flanagan,J., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L., Kim,S.H., Lee,B., Lomocan,M.A., Mazda,P., Mok,M.S., Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Punch,D., Shnr,E., Twomey,B., Wan,K.H., Whitelaw,K.R., Yee,A., Zhang,R., Zieran,L.L. and Kimmel,B.		
TITLE	Sequencing of Drosophila chromosome 2L, region 26A5-26B5		
REFERENCE	Unpublished (1997)		
AUTHORS	2 (bases 1 to 174311)		
TITLE	Direct Submission		
JOURNAL	Submitted (29-MAY-1998) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, US		
COMMENT	Sequence submitted by: Berkeley Drosophila Genome Project Lawrence Berkeley National Laboratory, MS 64-121 Berkeley, CA 94720 For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive web site (http://fruitfly.berkeley.edu/sequence-archive.html) or send email to drosophila@hgc.lbl.gov . Library locations: 58 64, 21 63, 40 90. Location/Qualifiers 1..174311 /organism="Drosophila melanogaster" /mol_type="genomic DNA" /db_xref="taxon:7227"		
FEATURES			
source			

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(D118)"
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DS05973 (D122) extends from 46131 to 131165. P1 DS08584
(D118) extends from 129315 to 174311."

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Alignment Scores:
Pred. No.:      2,13e-32      Length:      174311
Score:          483.00      Matches:      107
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Best Local Similarity: 41.96%      Mismatches: 87
Query Match:      36.13%      Indels:      14
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QY      2 AlaArgProGlyMetClnuArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSerGly 21
Db      21538 TCACAGACGGATGAGCGGTGGCGAACAACATGGCTGGTAACAGGAGCCAGCGGA 21597
QY      22 GlyILeGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGlyCys 41
Db      21598 GGCATAGGCCCGCTTGCTCGGGCCATGATCGCGCTGGACTACGGGTGGTGGCCCTG 21657
QY      42 AlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysGlySerAlaGlyTyrPro 61
Db      21658 GCACGTGGGAGCCCAAGTTGAAGAGCTC---AGGAGAGTCTCCCCGGGAGCTGCAG 21714
QY      62 GlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMetPhe 81
Db      21715 GCGAACTTCATACCGGGCGGTGCGACGCTCCAGGAAGATCAGGTGCAGAGCTCTTT 21774
QY      82 SerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeuAla 101
Db      21775 GACTGGATCGAACGGGAGCTGGAGGGCGCGACGTGCTGCTGAACAATGCTGCATTACT 21834
QY      102 ArgProAspThrLeuLeuSerGlySer---ThrSerGlyTyrTrpLysAspMetPheAsnVal 120
Db      21835 CGCGAGACGGAATGGTCAACCGCGAGCATACGACAGAGCTTAAGAGAGTCTATAGACACC 21894
QY      121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
Db      21895 AACGTAATGGCGTGTATTTGGTGTACCGCGAGGCGTTCAATAACATGAACGCGAGGT 21954
QY      141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeu----- 158
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QY      159 -----ProLeuSerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeu 176
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QY      177 ThrGluGlyLeuArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIle 196
Db      22072 ACAGAGACATATCGGCAGGAATTTACAGTGCATCGAACAAATAATCCGGGTACTGGCATC 22131
QY      197 SerProGlyValValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLys 216
Db      22132 TGTCCTGGTGGGTGAACAGCAATCTTTC-----CCGGAAGAG 22170
QY      217 AlaAlaAlaThrTyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaVal 236
Db      22171 ATCCATTTTTACGTCAAAGACATGGCCAGATCGAACACGCGAACATTCGGCAGCAGTG 22230
QY      237 IleTyrValLeuSerThrProAlaHisIleGlnIleGlyAspIle 251
Db      22231 ATGTATGCTCTCGGAATCCGCGCTTCAGTTTCAGGTGAGCATATTC 22275

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AC092216	174832 bp	DNA	linear	INV 30-JUN-2001
Drosophila melanogaster, chromosome 2L, region 25F-26A, BAC clone BACR10M11, complete sequence.				
AC092216				
AC092216.1	GI:14578097			
HTG				
Drosophila melanogaster (fruit fly)				
Drosophila melanogaster				
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.				
1 (bases 1 to 174832)				
Celniker, S.E., Adams, M.D., Krommiller, B., Tyler, D., Wan, K.H., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Bonzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champs, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, K.A., Nunoo, J., Phouanavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirkas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.				
Sequencing of Drosophila chromosome 2L, region 25F-26A				
Unpublished				
2 (bases 1 to 174832)				
Celniker, S.E., Adams, M.D., Krommiller, B., Tyler, D., Wan, K.H., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Bonzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champs, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferriera, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, K.A., Nunoo, J., Phouanavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirkas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.				
Direct Submission				
Submitted (30-JUN-2001) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, US				
Sequence submitted by:				
Berkeley Drosophila Genome Project				
Lawrence Berkeley National Laboratory, MS 64-121 Berkeley, CA 94720				
This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgs@fruitfly.berkeley.edu .				
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ORIGIN				
Alignment Scores:				
Pred. No.:	2.13e-32	Length:	174832	
Score:	483.00	Matches:	107	
Percent Similarity:	60.39%	Conservative:	47	

AUTHORS
CONSTRM
TITLE
JOURNAL
REFERENCE
AUTHORS
CONSTRM
TITLE
JOURNAL
COMMENT
FEATURES
source

FlyBase
Direct Submission
Submitted (06-SEP-2002) University of California Berkeley, 539 Life Sciences Addition, Berkeley, CA 94720, USA
6 (bases 1 to 260673)

FlyBase
Direct Submission
Submitted (23-JAN-2003) University of California Berkeley, 539 Life Sciences Addition, Berkeley, CA 94720, USA
On Sep 16, 2002 this sequence version replaced gi:7297037.

Location/Qualifiers
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CDS
gene
mRNA

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Alignment Scores:
Pred. No.: 3,49e-32 Length: 260673
Score: 483.00 Matches: 107
Percent Similarity: 60.39% Conservative: 47
Best Local Similarity: 41.96% Mismatches: 87
Query Match: 36.13% Indels: 14
DB: 3 Gaps: 5

US-10-063-735-128 (1-260) x AE003612 (1-260673)

QY 2 AlaArgProGlyMetGluArgTyrArgAspArgLeuAlaLeuValThrGlyAlaSerGly 21
Db 112253 TCACAAGACGGCATGAGCGGTGGCAGAACAACTGGTGTGTACAGGAGCCGCGGA 112194
QY 22 GlyIleGlyAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGlyCys 41
Db 112193 GCATAGGCCCGCGCTGTGCTCGGCCATGATCGGCGCTGGACTAGGGGTGTGGCCCTG 112134
QY 42 AlaArgThrValGlyAsnIleGluLeuAlaAlaGluCysLysSerAlaGlyTyrPro 61
Db 112133 GCACGTGGGAGCCCAAGTTGAAGAGCTC---AGGAGAGTCTGCCCGGAGCTGCAG 112077
QY 62 GlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMetPhe 81
Db 112076 GCGAACTTCATACCGCGCGCTGCCGCTCTCAAGAGAGATCAGTGCAGAGCTCTTT 112017
QY 82 SerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeuAla 101
Db 112016 GACTGTATCGAAGGAGCTGAGGGCGCGCTGCTCTGACATCTGTCATTACT 111957
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Db      111956 CGCGAGACGGAACCTGGTCAACCCGAGCAATACGAGAAAGCTTAAGGAGGTATAGACACC 111897
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Db      111896 AACGTAAATGGCGGTGATTGGTGTATACCCGCGAGCGGTTCAATAACATGAACGCGGAGGT 111837
QY      141 ValAspAspGlyHisIleAsnIleAsnSerMetSerGlyHisArgValLeu----- 158
Db      111836 ---GGCGAAGTCACTGCTCATCATCAACAGCATAGCCGACATCAGTGTCTCAACTTC 111780
QY      159 -----ProLeuSerValThrHisPheTyrSerAlaThrIleTyrAlaValThrAlaLeu 176
Db      111779 ATCGACGTTTTGCCATCGTTCAATATATATATCCGCCACCAAGTTTGCATCACCGCCATC 111720
QY      177 ThrGluGlyLeuArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIle 196
Db      111719 ACAGAGACATATCGCGCAGGAATTTTCAGCTGCACCTCGAACAAATCCCGGTTACTGGCATC 111660
QY      197 SerProGlyValValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLys 216
Db      111659 TGTCTGGTGGCGGTGAACACGAAATCTTC-----CCGGAAGAG 111621
QY      217 AlaAlaAlaThrTyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaVal 236
Db      111620 ATCCATTTTACGTCAAAGACATGCCAGACTCGCAACAGCGAATCGGAGCGCATG 111561
QY      237 IleTyrValLeuSerThrProAlaHisIleGlnIleGlyAspIle 251
Db      111560 ATGATATGCTTCGCAACTCGCCTCATGTTCCAGTGTAGCATAATC 111516

RESULT 14
AY094912
LOCUS   AY094912 1050 bp mRNA linear INV 15-APR-2002
DEFINITION Drosophila melanogaster RH17287 full insert cDNA.
ACCESSION AY094912
VERSION   AY094912.1 GI:20151810
KEYWORDS  FLY CDNA.
SOURCE    Drosophila melanogaster (fruit fly)
ORGANISM  Drosophila melanogaster
          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
          Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
          Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 1050)
          Stapleton,M., Brokstein,P., Hong,L., Agbayani,A., Carlson,J.,
          Champe,M., Chavez,C., Dorsett,V., Dresnek,D., Faifan,D., Frise,E.,
          George,R., Gonzalez,M., Guarin,H., Kronmiller,B., Li,P., Liao,G.,
          Miranda,A., Mungall,C.J., Nunco,J., Pacleb,J., Paragas,V., Park,S.,
          Patel,S., Phouanavong,S., Wan,K., Yu,C., Lewis,S.E., Rubin,G.M.
          and Celniker,S.
          Direct Submission
          Submitted (03-APR-2002) Berkeley Drosophila Genome Project,
          Lawrence Berkeley National Laboratory, One Cyclotron Road,
          Berkeley, CA 94720, USA
          Sequence submitted by:
          Berkeley Drosophila Genome Project
          Lawrence Berkeley National Laboratory
          Berkeley, CA 94720
          This clone was sequenced as part of a high-throughput process to
          sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
          Science 2000). The sequence has been subjected to integrity checks
          for sequence accuracy, presence of a polyA tail and contiguity
          within 100 kb in the genome. Thus we believe the sequence to
          reflect accurately this particular cDNA clone. However, there are
          artifacts associated with the generation of cDNA clones that may
          have not been detected in our initial analyses such as internal
          priming, priming from contaminating genomic DNA, retained introns
          due to reverse transcription of unspliced precursor RNAs, and
          reverse transcriptase errors that result in single base changes.
          For further information about this sequence, including its location
          and relationship to other sequences, please visit our Web site
          (http://fruitfly.berkeley.edu) or send email to
          cdna@fruitfly.berkeley.edu.

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FEATURES

source

Location/Qualifiers

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ORIGIN

Alignment Scores:

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Pred. No.: 4,93e-35 Length: 1050
Score: 482.00 Matches: 104
Percent Similarity: 62.26% Conservative: 56
Best Local Similarity: 40.47% Mismatches: 79
Query Match: 36.05% Gaps: 18
DB: 3

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US-10-063-735-128 (1-260) x AY094912 (1-1050)

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QY      26 AlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGlyCysAlaArgThrVal 45
Db      169 GCTGTGTGCAGGATTTGGTGTCAAGGCTTGTGTCTGTGGTCTTTGACGCTCGCGAG 228
QY      46 GlyAsnIleGluGluLeuAlaAlaGluCys-----LysSerAlaGlyTyrProGly 62
Db      229 GACCGCTGCGAGGAGCTGAAGGCTTCGCTCCAGCGGACGAGCCAGCTCGTTCCATGGA 288
QY      63 ThrLeuIleProTyrArgCysAspLeuSerAsnGluLysAspIleLeuSerMetPheSer 82
Db      289 CGC-----AAATGCGATGTGAGCCAGGAGGAGGTGATCGATGCGTTCGCA 336
QY      83 AlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeuAlaArg 102
Db      337 TGGATCGATGCAACACTGGCGGTGCGGATGCTCTGTCGATCTTCGTCATTCGGATACC 396
QY      103 ProAspThrLeuLeuSer-----GlySerThrSerGlyTyrIlePheAspMetPheAsnVal 120
Db      397 CTCGGTGTGGGCATCACCCAGAGGTAATGGCGCTGATCTTCGTCCTTCGATACC 456
QY      121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
Db      457 ATGTCTCTGGCGGTTTCTGGTGTGACCCGCGAGGCTTTCAAAATCACTGAAGACGCAAT 516
QY      141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeu----- 158
Db      517 GTTACGATGGACACATCTGATGTCAACAGTGTGGCCGACACCGGTTGATCAACAAC 576
QY      159 ProLeuSerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGlu 178
Db      577 CCAGGCATCACCATGGCGATGATTCCGCCATCGAAGTACGAGTACCCGCTCTCAGGAG 636
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Db 637 GTGCTGGTCCAGAGTTCACACCAACAGACCACAGGATTACAGCATCGTCCC 696
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Db 736 GTTGGCATTCCTGCTCCGCTCTGAGGATGTGGCCGATGCAATAGCTAC 795
Qy 239 ValLeuSerThrProAlaHisIleGlnLeuAspIleGlnMetArgPro 255
Db 796 TGCATCCAGACCCCGCCCAATGTCAGATTCACAGCTGACCATCAAGCCT 846

RESULT 15
AC017403/c 24222 bp DNA linear HTG 09-DEC-1999
LOCUS Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***.
DEFINITION AC017403
ACCESSION AC017403
VERSION AC017403.1 GI:6553583
KEYWORDS HTG; HTGS PHASE2.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 24222)
AUTHORS Adams,M. and Venter,J.C.
TITLE Direct Submission
JOURNAL Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
COMMENT This sequence was identified as CDM:10210603 by the submitter.
For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

FEATURES
source
1..24222
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
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ORIGIN
Alignment Scores:
Pred. No.: 2.82e-30 Length: 24222
Score: 448.50 Matches: 105
Percent Similarity: 56.14% Conservative: 55
Best Local Similarity: 36.84% Mismatches: 79
Query Match: 33.55% Indels: 46
DB: 2 Gaps: 6

US-10-063-735-128 (1-260) x AC017403 (1-24222)
Qy 6 MetGluArgTTPArgAspArgLeuAlaLeuValThrGlyAlaSerGlyGlyLeuGlyAla 25
Db 8151 ATGGATCTGTGGCTAAATCGCGTGTCTGTGTCTGCTGGCGCAGTTCGGGAATCGAGCT 8092
Qy 26 AlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGlyCysAlaArgThrVal 45
Db 8091 GCCTGTTCCAGGATTGCTGTCACAGGCTTGGTGTCTGGTCTGTCACGCTCGCGAG 8032
Qy 46 GlyAsnIleGluGluLeuAlaAlaGluCys-----LysSerAlaGlyTyrProGly 62
Db 8031 GACCGTCTGCAGAGCTGAAGGCTTCGCTGCCAGCGGACCCAGGCCAGTCGTTTCATGGA 7972
Qy 63 ThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMetPheSer 82
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Db 7863 CTCGGTGTGGGCATCACCCACGAGGTAATGGCGCTGATCTTGTGCGCATCTCGATACC 7804
Qy 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
Db 7803 AATGCTCTGGCGCTTGTGCTGCACCCGCGAGGCTTCAATCACTGAAGAGCGCAAT 7744
Qy 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeu----- 158
Db 7743 GTTAAACGATGGACACATCTGATTTGTCAACAGTGTGGCGGACACCCGGTGTATCAACA 7684
Qy 159 ProLeuSerValThrHisPheThrSerAlaThrIlystYrAlaValThrAlaLeuThrGlu 178
Db 7683 CCAGGCATCCATCGGCATGTATTCCCATTCGGAAGTACCGAGTCACCGCTCTCCAGG 7624
Qy 179 GlyLeuArgGlnGluLeuArgGluAlaGlnThr----- 189
Db 7623 GTGCTGCTCAGGAGTTCACACACACAGACCCACAGATTCACGGTAAGTGGCGAG 7564
Qy 190 -----HisIle 191
Db 7563 AGAGAGATTAGCTTAAAGTTGACATTCGATTACCCCTTTTCCGATAATAATATCATGT 7504
Qy 192 ArgAlaThr-CysIleSerProGlyValValGluThrGlnPheAlaPheLysLeuHisAs 211
Db 7503 GATTTTACAGAGCATCATGCTCCCGTGCCTGGACACCGAGATCATCGACAAG----- 7452
Qy 211 pLysAspProGluLysAlaAlaAlaThrTyrGluGlnMetLysCysLeuLysProGluAs 231
Db 7451 -----GAGGCTCTCGTTGGCATTCGCCGACTTTTCCAATGCTCCGCTCTGAGGA 7405
Qy 231 pValAlaGluAlaValIleTyrValLeuSerThrProAlaHisIleGlnIleGlyAspI 251
Db 7404 TGTGGCGGATGCCATTTAGCTACTGCTATCCAGACCCCGCCAAATGTCCAGATTCCAGGCT 7345
Qy 251 eGlnMetArgPro 255
Db 7344 GACCATCAAGCCT 7332

Search completed: September 16, 2004, 17:43:06
Job time : 3243 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 16, 2004, 16:26:21; Search time 356 Seconds

(without alignments)
3102.617 Million cell updates/sec

Title: US-10-063-735-128

Perfect score: 1337

Sequence: 1 MARPGMERWRDLALVTGAS.....STPAHQIGDIQMRPTEQVT 260

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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-NO MMAP -IARGUEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002s.*
7: Geneseqn2003as.*
8: Geneseqn2003bs.*
9: Geneseqn2003cs.*
10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1337	100.0	1493	9 ADB47522	ADB47522 Human CDN
2	1337	100.0	1505	4 AAS46113	AAS46113 Human DNA
3	1337	100.0	1505	4 AAF92121	AAF92121 Human PRO
4	1337	100.0	1505	6 ABS74441	ABS74441 Human CDN
5	1337	100.0	1505	7 ABX78716	ABX78716 Human PRO
6	1337	100.0	1505	7 ACA75688	ACA75688 Novel hum
7	1337	100.0	1505	7 ACA71168	ACA71168 Human sec
8	1337	100.0	1505	7 ACC87696	ACC87696 Human sec

9	1337	100.0	1505	7	ACC87082	Acc87082 Human sec
10	1337	100.0	1505	7	ACD04255	ACD04255 Human sec
11	1337	100.0	1505	7	ACA69586	ACA69586 CDNA enco
12	1337	100.0	1505	7	ACA90431	ACA90431 Novel hum
13	1337	100.0	1505	7	ACC89538	ACC89538 Human sec
14	1337	100.0	1505	7	ACA98329	ACA98329 Novel hum
15	1337	100.0	1505	7	ACA93971	ACA93971 Human sec
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18	1337	100.0	1505	7	ACF96871	ACF96871 Human sec
19	1337	100.0	1505	7	ACF15592	ACF15592 Human sec
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22	1337	100.0	1505	7	ACD01946	ACD01946 Novel hum
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24	1337	100.0	1505	7	ACA89563	ACA89563 CDNA enco
25	1337	100.0	1505	7	ACA73573	ACA73573 Human sec
26	1337	100.0	1505	7	ACA05888	ACA05888 Human sec
27	1337	100.0	1505	7	ACA66722	ACA66722 CDNA enco
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37	1337	100.0	1505	7	ACA72345	ACA72345 Novel hum
38	1337	100.0	1505	7	ACD04869	ACD04869 Novel hum
39	1337	100.0	1505	7	ACD18330	ACD18330 Human sec
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45	1337	100.0	1505	7	ACD15978	ACD15978 Human sec

ALIGNMENTS

RESULT 1

ADB47522

ID: ADB47522 standard; CDNA; 1493 BP.

XX ADB47522;

AC ADB47522;

DT 04-DEC-2003 (first entry)

XX Human CDNA upregulated in dendritic cells SEQ ID NO 222.

DE ss; gene; human; dendritic cells; high throughput; cancer;

XX KW infectious disease; autoimmune disease; allergy;

XX KW graft versus host disease; vaccine enhancing; gene therapy.

XX OS Homo sapiens.

XX US2003134283-A1.

PN 17-JUL-2003.

XX 03-OCT-2001; 2001US-00971392.

XX 03-OCT-2000; 2000US-0237652P.

XX (PETE/) PETERSON D P.

XX (PEAR/) PEARSON C I.

XX (COCK/) COCKS B G.

XX Peterson DP, Pearson CI, Cocks BG;

XX WPI; 2003-662509/62.

PT New combination comprises cDNAs that are differentially expressed in
PT dendritic cells useful for preparing a composition for diagnosing or
PT treating cancer, infectious disease, autoimmunity, allergy or graft
PT versus host disease.
XX
XX Claim 1; SEQ ID NO 222; 28pp; English.
XX
CC The invention relates to a combination comprising cDNAs that are
CC differentially expressed in dendritic cells (DC). Also included is a high
CC throughput method for detecting differential expression of one or more
CC cDNAs in a sample containing nucleic acids. The combination is useful for
CC preparing a composition for diagnosing, treating and monitoring the
CC treatment of cancer, infectious disease, autoimmunity, allergy or graft
CC versus host disease, or for enhancing a vaccine. The present sequence
CC represents a human cDNA upregulated in dendritic cells. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?docID=20030134283.
XX
XX SQ Sequence 1493 BP; 297 A; 442 C; 419 G; 335 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2,32e-128 Length: 1493
Score: 1337.00 Matches: 260
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-10-063-735-128 (1-260) x ADB47522 (1-1493)

Qy 1 MetAlaArgProGlyMetGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSer 20
Db 112 ATGCCAGCCGCGCATGAGCGGTGGCGCACCGCGTGGTGGTACCGGGGCGCTCG 171
Qy 21 GlyGlyLeuGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly 40
Db 172 GGGGGCATCGGGCGCGCGTGGCGCGCGCTGGTCCAGAGGAGACTGAAGTGGTGGGC 231
Qy 41 CysAlaArgThrValGlyAsnIleGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
Db 232 TGGCGCCGCACCTGTGGGCACATCAGAGAGTGGTGTGAATGTAAGTGCAGGCTAC 291
Qy 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet 80
Db 292 CCCGGGACTTGTATCCCTACAGATGTGACCTATCAATGAAGAGGACATCTCTCCATG 351
Qy 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeu 100
Db 352 TTCTCAGTATCCGTCTCAGCACAGCGGTGTAGACATCTGCATCAACAATGCTGGCTTG 411
Qy 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnVal 120
Db 412 CCGCGGCGCTGACACCTCTCTCAGGACAGCAGTGGTGGTGAAGGACATGTTCAATGTG 471
Qy 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
Db 472 AACGTGCTGGCGCCTCAGCATCTGCACAGGGAAGCCTACCATGTCATGAAGAGCGGAAT 531
Qy 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
Db 532 GTGGAGCATGGGCACATCAATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTG 591
Qy 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
Db 592 TCTGTGACCCACTTCTATAGTGCACCAAGATGCGGTCACTGGCGCTGACAGAGGAGTGTG 651
Qy 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
Db 652 AGGCAGAGCTTGGGAGGCCAGACCACATCCGAGCCACGTGCATCTCTCCAGGTGTG 711
Qy 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLeuAlaAlaThr 220

Db 712 GTGAGACACAAATTCGCTTCAAACTCCACGACAGGACCTCGAGAAAGGACGCTGCCACC 771
Qy 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
Db 772 TATGAGCAAAATGAAGTGTCTCAAAACCGAGGATGTGGCCGAGGCTGTATCTACGTCCTC 831
Qy 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
Db 832 AGCACCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCCGGAGGAGGTGACC 891
RESULT 2
ID AAS46113 standard; cDNA; 1505 BP.
XX AAS46113;
AC AAS46113;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human DNA encoding PRO polypeptide sequence #189.
XX
KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;
KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;
KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;
KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
KW PCR primer.
XX
OS Homo sapiens.
XX
XX WO200168848-A2.
XX
XX 20-SEP-2001.
XX
XX 28-FEB-2001; 2001WO-US006520.
XX
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 06-MAR-2000; 2000US-0186968P.
PR 14-MAR-2000; 2000US-0189320P.
PR 14-MAR-2000; 2000US-0189328P.
PR 15-MAR-2000; 2000WO-US006884.
PR 21-MAR-2000; 2000US-0190828P.
PR 21-MAR-2000; 2000US-0191007P.
PR 21-MAR-2000; 2000US-0191048P.
PR 21-MAR-2000; 2000US-0191314P.
PR 28-MAR-2000; 2000US-0192655P.
PR 29-MAR-2000; 2000US-0193032P.
PR 29-MAR-2000; 2000US-0193053P.
PR 30-MAR-2000; 2000WO-US008439.
PR 04-APR-2000; 2000US-0194449P.
PR 04-APR-2000; 2000US-0194647P.
PR 11-APR-2000; 2000US-0195975P.
PR 11-APR-2000; 2000US-0196000P.
PR 11-APR-2000; 2000US-0196187P.
PR 11-APR-2000; 2000US-0196690P.
PR 11-APR-2000; 2000US-0196820P.
PR 18-APR-2000; 2000US-0198121P.
PR 18-APR-2000; 2000US-0198585P.
PR 25-APR-2000; 2000US-0199397P.
PR 25-APR-2000; 2000US-0199550P.
PR 25-APR-2000; 2000US-0199654P.
PR 03-MAY-2000; 2000US-0201516P.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 22-AUG-2000; 2000US-00644848.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000WO-US034956.

XX PA (GETH) GENENTECH INC.

XX PI Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;

XX PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

XX DR WPI; 2001-602746/68.

XX DR P-PSDB; AAU29212.

XX PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the

XX PT presence of tumors, such as prostate and breast tumors, in mammals and to

XX PT screen for modulators of the compounds.

XX PS Claim 2; Fig 377; 774pp; English.

XX CC Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR

XX CC primers for PRO polypeptides of the invention. The sequences of the

XX CC invention can be used to detect the presence of a tumour in a mammal by

XX CC comparing the level of expression of a PRO polypeptide in a test sample

XX CC of cells from the animal and a control sample of normal cells, whereby a

XX CC higher level of expression in the test sample indicates the presence of a

XX CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,

XX CC pigs, goats and rabbits but are preferably human. The polypeptides can be

XX CC used to stimulate tumour necrosis factor (TNF) alpha release from human

XX CC blood, when contacted with it. A specific polypeptide can be used to

XX CC stimulate the proliferation or differentiation of chondrocyte cells. The

XX CC PRO proteins can be used to determine the presence of tumours and also

XX CC susceptibility to tumour development, particularly adrenal, lung, colon,

XX CC breast, prostate, rectal, cervical, or liver tumours, in mammalian

XX CC subjects. The oligonucleotide probes specific for the PRO nucleic acids

XX CC can be used for genetic analysis of individuals with genetic disorders

XX SQ Sequence 1505 BP; 309 A; 442 C; 419 G; 335 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 2.35e-128 Length: 1505

Score: 1337.00 Matches: 260

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 4 Gaps: 0

US-10-063-735-128 (1-260) x AAS46113 (1-1505)

QY 1 MetAlaArgProGlyMetGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSer 20

DB 112 ATGCCAGCGCCGGCATGGAGCGTGGCGGCGACCGCGCTGGTGGACGGGGCGCTCG 171

QY 21 GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly 40

DB 172 GGGGGCATCGCGCGCGCGTGGCGCGGCGCTGGTCCAGCAGGAGCTGAAGTGGTGGGC 231

QY 41 CysAlaArgThrValGlyAsnIleGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60

DB 232 TGCCTCCGCGCATGTGGGCAACATCCAGGAGTGGCTGCTGAATGTAAGAGTGCGAGGTAC 291

QY 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluAlaAspIleLeuSerMet 80

DB 292 CCCGGGACATTTGATCCCCCTCAGATGTGACCTATCAATGAAGAGGACATCTCTCCATG 351

QY 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu 100

DB 352 TTCTCAGTATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACATGCTGGCTTG 411

QY 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnVal 120

DB 412 GCCCGGCGTCACACCTGCTCTCAGGAGCAGCAGTGGTGGAGGACATGTTCAATGTG 471

QY 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140

DB 472 AACGTGTGGCCCTCAGCATCTGCACAGCGGAGCCCTACCATGTCATGAGGAGCGGAAT 531

QY 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160

DB 532 GTGACGATGGGCATCATTAATCAATAGCATGCTGGCCACCGAGTGTATCCCTG 591

QY 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180

DB 592 TCTGTGACCCACTTCTATAGTGGCCACCAAGTATGCCGTCACTGGCTGCAGAGGACTG 651

QY 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200

DB 652 AGGCAAGAGCTTCGGGAGGCCAGACCCACATCCGAGCCAGTGCATCTCTCCAGGTGTG 711

QY 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaThr 220

DB 712 GTGAGACACAAATTCGCTTCAAACTCCACAGAGGACCTGAGAGCGAGTCCACCC 771

QY 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240

DB 772 TATGAGCAATGAAGTGTCTCAACCCGAGGATGTGGCCGAGGCTGTATCTACGTCCTC 831

QY 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260

DB 832 AGCACCCCGCACATCCAGATTGGAGACATCCAGATGAGGCCACCGAGCGAGGTGACC 891

RESULT 3

AAF92121

ID AAF92121 standard; cDNA; 1505 BP.

XX AC AAF92121;

XX DT 15-MAY-2001 (first entry)

XX DE Human PRO1774 cDNA.

XX KW Human; PRO protein; mapping; ss.

XX OS Homo sapiens.

XX PN WO200116318-A2.

XX PD 08-MAR-2001.

XX PF 24-AUG-2000; 2000WO-US023328.

XX PR 01-SEP-1999; 99WO-US020111.

XX PR 15-SEP-1999; 99WO-US021090.

XX PR 07-DEC-1999; 99US-0169495P.

XX PR 09-DEC-1999; 99US-0170262P.

XX PR 11-JAN-2000; 2000US-0175481P.

XX PR 18-FEB-2000; 2000WO-US004341.

XX PR 18-FEB-2000; 2000WO-US004342.

XX PR 22-FEB-2000; 2000WO-US004414.

XX PR 01-MAR-2000; 2000WO-US005601.

XX PR 03-MAR-2000; 2000US-0187202P.

XX PR 21-MAR-2000; 2000US-0191007P.

XX PR 30-MAR-2000; 2000WO-US008439.

XX PR 25-APR-2000; 2000US-0199397P.

XX PR 22-MAY-2000; 2000WO-US014042.

XX PR 05-JUN-2000; 2000US-0209832P.

(GETH) GENENTECH INC.

XX PA Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;

XX PI Grimaldi CJ, Gurney AL, Watanabe CK, Wood WI;

XX DR WPI; 2001-183260/18.

XX DR P-PSDB; AAB87589.

XX PT Eighty four nucleic acids encoding PRO polypeptides, useful in molecular

XX PT biology, including use as hybridization probes, and in chromosome and

XX PT gene mapping.

XX PS Claim 2; Fig 127; 278pp; English.

CC The present sequence is the coding sequence for a human PRO polypeptide
 CC (secreted and transmembrane). The PRO protein, and PRO agonists, PRO
 CC antagonists or anti-PRO antibodies are useful for preparation of a
 CC medicament useful in the treatment of a condition which is responsive to
 CC the PRO protein, agonists, antagonists or anti-PRO antibodies. The PRO
 CC protein may also be employed as molecular weight markers for protein
 CC electrophoresis. The PRO coding sequence has applications in molecular
 CC biology, including use as hybridisation probes, and in chromosome and
 CC gene mapping

XX SQ Sequence 1505 BP; 309 A; 442 C; 419 G; 335 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,35e-128	Length:	1505
Score:	1337.00	Matches:	260
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	4	Gaps:	0

US-10-063-735-128 (1-260) x AAF92121 (1-1505)

QY	1	MetAlaArgProGlyMetGluArgTyrArgAspArgLeuAlaLeuValThrGlyAlaSer	20
DB	112	ATGCCAGCCCGGCATCGAGCGTGGCGCGACCGCTGGCGTGGTACGGGGGCTCG	171
QY	21	GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuValValGly	40
DB	172	GGGGGATCGCGCGCGCGTGGCGCGGCGCTGGTCCAGCGGACTGAAGTGGTGGGC	231
QY	41	CysAlaArgThrValGlyAsnIleGluLeuAlaAlaGluCysLysSerAlaGlyTyr	60
DB	232	TGCGGCCCACTGGGGCAACATCAGAGGTGGCTGTGAATGTAAAGTGCAGGCTAC	291
QY	61	ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet	80
DB	292	CCCGGGATTGTATCCCTACAGATGTGACCTATCAATGAAGAGCATCTCTCCATG	351
QY	81	PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeu	100
DB	352	TTCTCAGTATCCGTTCTCAGCACAGCGTGTAGACATCTGCATCAACAATGCTGGCTG	411
QY	101	AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnVal	120
DB	412	GCCCGGCTGACACCTGCTCTCAGGCAGCACCATGTTGAAGAGCATGTTCAATGTG	471
QY	121	AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn	140
DB	472	AACGTGTGGCTCAGCATCTGCACCGGAAGCTTACCAGTCCATGAAGGAGCGGAAT	531
QY	141	ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu	160
DB	532	GTGGACGATGGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTG	591
QY	161	SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu	180
DB	592	TCTGTGACCCACTCTATAGTCCACCAAGTATGCCGTACCTGCGTCCAGAGGACTG	651
QY	181	ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal	200
DB	652	AGGCAAGAGCTTCGGGAGGCCAGACCCACATCCGAGCCACGTGCATCTCTCCAGTGTG	711
QY	201	ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaThr	220
DB	712	GTGGAGACACAATTGCGCTTCAAACTCCACGAAAGGACCCCTGAGAAGCGAGCTGCCACC	771
QY	221	TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu	240
DB	772	TATGAGCAAAATGAAGTGTCTCAAAACCGAGGATGGCCGAGGCTGTTATCTACGCTCTC	831
QY	241	SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr	260
DB	832	AGCACCCCGCACATCATCAGATTGGAGACATCCAGATGAGGCCACCGAGCGAGTGACC	891

RESULT 4	
ABS74441	
ID	ABS74441 standard; cDNA; 1505 BP.
XX	AC ABS74441;
XX	DT 10-DEC-2002 (first entry)
XX	DE Human cDNA encoding secreted/transmembrane protein PRO1774.
KW	Human; ss; Gene; secreted protein; transmembrane protein; antirheumatic;
KW	antiarthritic; osteopathic; sports-related joint problem;
KW	articular cartilage defect; osteoarthritis; rheumatoid arthritis.
OS	Homo sapiens.
XX	US2002119130-A1.
XX	29-AUG-2002.
XX	06-DEC-2001; 2001US-00006867.
PR	29-OCT-1997; 97US-0063435P.
PR	29-OCT-1997; 97US-0064215P.
PR	22-APR-1998; 98US-0082737P.
PR	29-APR-1998; 98US-0083495P.
PR	15-MAY-1998; 98US-0085579P.
PR	02-JUN-1998; 98US-0087759P.
PR	04-JUN-1998; 98US-0088021P.
PR	04-JUN-1998; 98US-0088029P.
PR	04-JUN-1998; 98US-0088030P.
PR	10-JUN-1998; 98US-0088734P.
PR	10-JUN-1998; 98US-0088740P.
PR	10-JUN-1998; 98US-0088811P.
PR	10-JUN-1998; 98US-0088824P.
PR	10-JUN-1998; 98US-0088825P.
PR	11-JUN-1998; 98US-0088863P.
PR	12-JUN-1998; 98US-0089105P.
PR	16-JUN-1998; 98US-0089514P.
PR	17-JUN-1998; 98US-0089653P.
PR	19-JUN-1998; 98US-0089952P.
PR	22-JUN-1998; 98US-0090246P.
PR	24-JUN-1998; 98US-0090444P.
PR	25-JUN-1998; 98US-0090688P.
PR	25-JUN-1998; 98US-0090696P.
PR	26-JUN-1998; 98US-0090862P.
PR	02-JUL-1998; 98US-0091628P.
PR	10-AUG-1998; 98US-0096012P.
PR	17-AUG-1998; 98US-0096757P.
PR	18-AUG-1998; 98US-0096949P.
PR	18-AUG-1998; 98US-0096959P.
PR	26-AUG-1998; 98US-0097954P.
PR	26-AUG-1998; 98US-0097971P.
PR	01-SEP-1998; 98US-0097979P.
PR	01-SEP-1998; 98US-0098743P.
PR	10-SEP-1998; 98US-0099741P.
PR	10-SEP-1998; 98US-0099763P.
PR	10-SEP-1998; 98US-0099792P.
PR	10-SEP-1998; 98US-0099812P.
PR	10-SEP-1998; 98US-0099815P.
PR	16-SEP-1998; 98US-0100627P.
PR	16-SEP-1998; 98US-0100662P.
PR	16-SEP-1998; 98US-0100683P.
PR	17-SEP-1998; 98US-0100684P.
PR	17-SEP-1998; 98US-0100930P.
PR	22-SEP-1998; 98US-0101279P.
PR	23-SEP-1998; 98US-0101475P.
PR	24-SEP-1998; 98US-0101738P.
PR	24-SEP-1998; 98US-0101743P.
PR	24-SEP-1998; 98US-0101916P.
PR	30-SEP-1998; 98US-0102570P.

PR 06-OCT-1998; 98US-0103449P.
 PR 08-MAR-1999; 99WO-US005028.
 PR 14-MAY-1999; 99WO-US010733.
 PR 02-JUN-1999; 99WO-US012252.
 PR 01-SEP-1999; 99WO-US020111.
 PR 15-SEP-1999; 99WO-US021030.
 PR 15-SEP-1999; 99WO-US021194.
 PR 22-DEC-1999; 99WO-US031070.
 PR 18-FEB-2000; 2000WO-US004341.
 PR 18-FEB-2000; 2000WO-US004342.
 PR 22-FEB-2000; 2000WO-US004414.
 PR 01-MAR-2000; 2000WO-US005601.
 PR 30-MAR-2000; 2000WO-US005601.
 PR 22-MAY-2000; 2000WO-US014042.
 PR 02-JUN-2000; 2000WO-US015264.
 PR 23-AUG-2000; 2000WO-US023522.
 PR 24-AUG-2000; 2000WO-US023328.
 PR 10-NOV-2000; 2000WO-US030873.
 PR 01-DEC-2000; 2000WO-US032378.
 PR 20-DEC-2000; 2000WO-US034956.
 PR 28-FEB-2001; 2001WO-US006520.
 PR 01-MAR-2001; 2001WO-US006666.
 PR 30-MAY-2001; 2001WO-US017443.
 PR 01-JUN-2001; 2001WO-US017800.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 29-JUN-2001; 2001WO-US021066.
 PR 09-JUL-2001; 2001WO-US021735.

XX (GETH) GENENTECH INC.

XX Eaton DL, Filvaroff E, Gerritsen ME, Goddard A, Godowski PJ;

PI Grimaldi JC, Gurney AL, Watanabe CK, Wood WI;

DR WPI; 2002-731348/79.

DR P-PSDB; ABG95914.

PT New isolated secreted and transmembrane PRO polypeptide useful for
 PT modulating biological activity of a cell, or for treating sports-related
 PT joint problems, osteoarthritis or rheumatoid arthritis.

XX Claim 2; Fig 127; 399pp; English.

XX The invention relates to an isolated secreted and transmembrane PRO
 CC polypeptide having 80 % sequence identity to a sequence appearing as
 CC ABG95914-ABG95934 or their associated signal peptide, or a sequence of an
 CC extracellular domain of the proteins with their associated signal peptide
 CC or lacking its associated signal peptide. Also included are the nucleic
 CC acids encoding the proteins, vectors, host cells, fusion proteins and
 CC antibodies which specifically bind to the proteins. The proteins are
 CC useful for detecting a polypeptide designated as A, B, C or D in a sample
 CC suspected of containing an A, B, C or D polypeptide, by contacting the
 CC sample with a polypeptide designated as E, F, G, H or I (or vice versa)
 CC and determining the formation of a A/E, B/F, C/G, D/H or E/I polypeptide
 CC conjugate in the sample, where the formation of the conjugate is
 CC indicative of the presence of an A, B, C or D polypeptide in the sample,
 CC where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a
 CC PRO10096 polypeptide, D is a PRO19760 polypeptide, E is a PRO5901
 CC polypeptide, F is a PRO1 polypeptide, G is a PRO20040 polypeptide, H is a
 CC a cell suspected of expressing the A, B, C or D polypeptide. The sample comprises
 CC H or I polypeptide is labeled with a detectable label or is attached to a
 CC solid support. The proteins are useful for linking a bioactive molecule
 CC to a cell expressing a polypeptide designated as A, B, C or D or E, F, G,
 CC H or I. The bioactive molecule is a toxin, a radiolabel or an antibody.
 CC The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H,
 CC or I, or antibodies against them are useful for modulating a biological
 CC activity of a cell expressing a polypeptide designated as A, B, C or D or
 CC E, F, G, H, or I. The cell is killed. The proteins are useful for
 CC identifying agonists or antagonists, for the preparation of a medicament
 CC useful in the treatment of a condition which is responsive to the
 CC proteins, as molecular weight markers for protein electrophoresis
 CC purposes, and as therapeutic agents for treating sports-related joint
 CC problems, articular cartilage defects, osteoarthritis or rheumatoid

CC arthritis. Nucleic acids encoding the proteins are useful as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of anti-sense RNA and DNA, for the preparation of the proteins, to
 CC generate transgenic or knockout animals which are useful in the
 CC development and screening of therapeutic useful reagents, for chromosome
 CC identification, and in gene therapy. The antibody is useful as a
 CC therapeutic agent, in a diagnostic assay and for affinity purification of
 CC the protein from recombinant cell culture natural sources. The present
 CC sequence encodes a novel secreted or transmembrane protein of the
 CC invention

XX SQ Sequence 1505 BP; 309 A; 442 C; 419 G; 335 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2,35e-128	Length:	1505
Score:	1337.00	Matches:	260
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-10-063-735-128 (1-260) x ABS74441 (1-1505)

Qy	1	MetAlaArgProGlyMetGluArgTyrArgAspArgLeuAlaLeuValThrGlyAlaSer	20
Db	112	ATGCCAGGCGCCGATGGAGCGGTGGCGCCGCCGCTGGCGCTGGTACGGGGCCCTCG	171
Qy	21	GlyGlyIleGlyAlaAlaValAlaAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly	40
Db	172	GGGGGCGATCGCGCGCGCGTGGCGCGGCTGGCGCGCCGCTGGCGCTGGTACGGGGCCCTCG	231
Qy	41	CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyr	60
Db	232	TGCGCCCGCATCTGTGGGCAACATCGAGGAGTGGCTGTAATTAAGAGTGCAGGCTAC	291
Qy	61	ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet	80
Db	292	CCGGGAGCTTGTATCCCTCAGATGTGACTATCAATGAAGAGGACATCCTCTCCATG	351
Qy	81	PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu	100
Db	352	TTCTCAGCTATCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACATGCTGGCTTG	411
Qy	101	AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnVal	120
Db	412	GCCCGGCTCAGACCCCTGCTCTCAGGAGCAGCAGCAGTGGTTGGAAGGACATGTTCAATGTG	471
Qy	121	AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn	140
Db	472	AACGTGCTGGCCCTCAGCAGCGGTGTAGACATCTGCATCAACATGCTGGCTTG	531
Qy	141	ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu	160
Db	532	GTGGACGATGGGACATCATTAACATCAATAGCATGTCTGCCACCGAGTGTATACCCCTG	591
Qy	161	SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu	180
Db	592	TCTGTGACCACTTCTATAGTGCACCAAGTATGCGCTCACTGCGCTGACAGAGGAGT	651
Qy	181	ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal	200
Db	652	AGGCAAGAGCTTCGGAGGCGCCAGCCACCATCCGAGCCACGTCGTCCTCAGAGGTG	711
Qy	201	ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGlyLysAlaAlaThr	220
Db	712	GTGGAGACAAATTCGCTTCAACTCCAGCAGCAGGACCCCTGAGAGGAGGAGTGCACC	771
Qy	221	TyrGluGlnMetLysCysLysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu	240
Db	772	TATGAGCAATGAATGTCTCTCAAAACCGAGGATGTGGCGGAGGTGTATCTACGTCTC	831
Qy	241	SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr	260

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KW	KW	liver; dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;	
KW	KW	antibody-dependent enzyme mediated prodrug therapy.	
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XX	PD	06-FEB-2003.	
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Pred. No.: 2,35e-128
Score: 1337.00
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DT 07-JUL-2003 (first entry)
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KW chondrocyte proliferation; chondrocyte differentiation; tumour;
KW adrenal tumour; lung tumour; colon tumour; breast tumour;
XX prostate tumour; rectal tumour; cervical tumour; liver tumour; gene; ss.
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PR	29-SEP-1998;	98US-0102240P.			
PR	29-SEP-1998;	98US-0102330P.			
PR	30-SEP-1998;	98US-0102331P.			
PR	30-SEP-1998;	98US-0102487P.			
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PR	01-OCT-1998;	98US-0102571P.			
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Alignment Scores:

Pred. No.: 2.35e-128

Score: 1337.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 7

DB: 1

US-10-063-735-128 (1-260) x ACA75688 (1-1505)

QY	1	MetAlaArgProGlyWecGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSer	20
Db	112	ATGCCAGCCCGGATGGAGCGGTGGCGCACCGGCTGGCGTGGTACGGGGGCTCG	171
QY	21	GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuIleValValGly	40
Db	172	GGGGGCATCGCGCGCGCCGTGGCCCGGCGCCCTGGTCCACAGGGACTGAAGTGTGGTGGC	231
QY	41	CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysIleValValGlyTyr	60
Db	232	TGCGCCCGCACTGTGGGCAACATCGAGAGCTGGCTGCTGANTGTAAGAGTGCAGGCTAC	291
QY	61	ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet	80
Db	292	CCCGGGACTTTGATCCCTTACAGATGTGACCTTATCAATGAAGAGACATCCTCTCCATG	351
QY	81	PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu	100
Db	352	TTCTCAGCTATCCGTTCTCAGCACAGCGGTGAGACATCTGCATCAACAATGCTGGCTTG	411
QY	101	AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrIleValAspMetPheAsnVal	120
Db	412	GCCCGGCTGACACCTCTCTCAGCAGCAGCAGTGGTGGAGGACATGTTCAATGTG	471
QY	121	AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetIleValArgAsn	140
Db	472	AACGTGTGGCCCTCAGCATCTGCACACGGGAAGCCTACCACTCCATGAAGAGCGGAAT	531
QY	141	ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu	160
Db	532	GTGACCATGGGCACATCAATCAATCAATAGCATGTCTGGCCACCGAGTGTACCCCTG	591

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PR 08-APR-1998; 98US-0081070P.
PR 09-APR-1998; 98US-0081195P.
PR 15-APR-1998; 98US-0081838P.
PR 21-APR-1998; 98US-0082568P.
PR 21-APR-1998; 98US-0082569P.
PR 22-APR-1998; 98US-0082704P.
PR 22-APR-1998; 98US-0082797P.
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PR 06-MAY-1998; 98US-0084414P.
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PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0098014P.
PR 01-SEP-1998; 98US-0098716P.
PR 01-SEP-1998; 98US-0098723P.
PR 02-SEP-1998; 98US-0098803P.
PR 02-SEP-1998; 98US-0098821P.
PR 02-SEP-1998; 98US-0098843P.
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PR 10-SEP-1998; 98US-0099741P.
PR 10-SEP-1998; 98US-0099754P.
PR 10-SEP-1998; 98US-0099763P.
PR 10-SEP-1998; 98US-0099812P.
PR 15-SEP-1998; 98US-0100388P.
PR 16-SEP-1998; 98US-0100662P.
PR 16-SEP-1998; 98US-0100664P.
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PR 29-SEP-1998; 98US-0102207P.
PR 29-SEP-1998; 98US-0102240P.
PR 29-SEP-1998; 98US-0102330P.
PR 29-SEP-1998; 98US-0102331P.
PR 30-SEP-1998; 98US-0102487P.
PR 30-SEP-1998; 98US-0102570P.
PR 30-SEP-1998; 98US-0102571P.
PR 01-OCT-1998; 98US-0102684P.
PR 01-OCT-1998; 98US-0102687P.

PR 02-OCT-1998; 98US-0102965P.
 PR 06-OCT-1998; 98US-0103258P.
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 PR 07-OCT-1998; 98US-00168978.

Alignment Scores:

Pred. No.: 2,35e-128 Length: 1505
 Score: 1337.00 Matches: 260
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-10-063-735-128 (1-260) x ACA71168 (1-1505)

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 QY 21 GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly 40
 Db 172 GGGGCGATCGCGCGCGCGTGGCGCGGCGCTGTCTCCAGCAGGACTGAAGGTGTGGGC 231
 QY 41 CysAlaArgThrValGlyAsnIleGluLeuAlaGluCysLysSerAlaGlyTyr 60
 Db 232 TCGCGCCGCACTGTGGGCAACATCGAGGAGCTGGCTGTAATGTAAGAGTCAGGCTAC 291
 QY 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluAspIleLeuSerMet 80
 Db 292 CCCGGGACTTTGATCCCTCAGATGTGACCTATCAATGAGAGGACATCTCTCCATG 351
 QY 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu 100
 Db 352 TTCTCAGTATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACAATGCTGGCTTG 411
 QY 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnVal 120
 Db 412 GCCCGGCTGACACCTGCTCTCAGGAGCAGCAGTGGTGTGAAGGACATGTTCAATGTG 471
 QY 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
 Db 472 AACGTGTGGCCCTCAGCATCTGCACAGCGGAGGAGCCTACCATGTCATGAGGAGCGGA 531
 QY 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
 Db 532 GTGGACGATGGGCATCATTTAAATCAATAGCATGTCTGGCCACCGAGTGTACCCCTG 591
 QY 161 SerValThrHisPheTyrSerAlaThrIlystTyrAlaValThrAlaLeuThrGluGlyLeu 180
 Db 592 TCTGTGACCACTTCTATAGTGCACCAAGTATGCCGTCACTGCGCTGACAGAGGACTG 651
 QY 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
 Db 652 AGGCAAGAGCTTCGGAGGCGCCAGACCCACATCCGAGCCAGCTGCATCTCTCCAGGTGTG 711
 QY 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThr 220
 Db 712 GTGGAGACAAATTCGCTTCAAACTCCACGACGAGGACCTGAGAGGCGACTGCCACC 771
 QY 221 TyrGlnGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
 Db 772 TATGAGCAATGAAGTGTCTCAAAACCCGAGGATGTGGCCGAGGCTGTATCTACGTCTC 831
 QY 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
 Db 832 AGCACCCCGCACACATCCGATTGGAGACATCCAGATGAGGCCCGGAGGAGGCTGACC 891

RESULT 8

ACC87696
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 AC ACC87696;
 XX

05-AUG-2003 (first entry)

Human secreted polypeptide PRO1774-encoding cDNA, SEQ ID NO:377.

Human; PRO; secreted protein; transmembrane protein;
 extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
 chondrocyte; proliferation; differentiation; cartilage disorder;
 bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
 adrenal tumour; lung; colon; breast; prostate; kidney; cervix;
 liver; drug screening; transgenic animal; genetic analysis;
 antiarthritic; vulnery; gene therapy; gene; ss.

Homo sapiens.

US2003027278-A1.

06-FEB-2003.

21-JUN-2002; 2002US-00176987.

18-SEP-1997; 97US-0059263P.
 18-SEP-1997; 97US-0059266P.
 17-OCT-1997; 97US-0062250P.
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 07-MAY-1998; 98US-0084639P.
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 15-MAY-1998; 98US-0085580P.
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PR	15-MAY-1998;	98US-0085700P.	PR	17-AUG-1998;	98US-0096897P.	Alignment Scores:	Pred. No.:	2.35e-128	Length:	1505
PR	18-MAY-1998;	98US-0086023P.	PR	18-AUG-1998;	98US-0096949P.	Score:		1337.00	Matches:	260
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PR	02-JUN-1998;	98US-0087759P.	PR	26-AUG-1998;	98US-0097971P.
PR	03-JUN-1998;	98US-0087827P.	PR	26-AUG-1998;	98US-0097974P.
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PR	04-JUN-1998;	98US-0088326P.	PR	02-SEP-1998;	98US-0098821P.
PR	05-JUN-1998;	98US-0088167P.	PR	02-SEP-1998;	98US-0098843P.
PR	05-JUN-1998;	98US-0088202P.	PR	03-SEP-1998;	98US-0098602P.
PR	05-JUN-1998;	98US-0088212P.	PR	10-SEP-1998;	98US-0099741P.
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Alignment Scores:
Pred. No.: 2,35E-128
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Length:
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Percent Similarity: 100.00% Conservative: 0
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OS Homo sapiens.

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Alignment Scores:
Pred. No.: 2,35e-128 Length: 1505
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US-10-063-735-128 (1-260) x ACA90431 (1-1505)

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DB 112 ATGGCCAGGCGCGCATGAGCGGTGGCGCGACCGCGCTGGCGTGGTACGGGGCGCTCG 171
QY 21 GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly 40
DB 172 GGGGCGATCGGCGCGCGCGTGGCGCGCGCGCGCGTGGTCCAGCAGGACTGAGAGTGTGGGC 231
QY 41 CysAlaArgThrValGlyAsnIleGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
DB 232 TGGCGCGCACCTGTGGGCAACATCAGGAGCTGGCTGCTGAATGTAAGAGTGCAGGCTAC 291
QY 61 ProGlyThrLeuIleProThrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet 80
DB 292 CCCGGGACTTTGATCCCTTACAGATGTGACCTATCAATGAAGAGGACATCTCTCCATG 351
QY 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeu 100
DB 352 TTCTCAGCTATCCGTTCTCAGCACAGCGGTGAGACATCTGCATCAACAATGCTGGCTTG 411
QY 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnVal 120
DB 412 GCCCGGCTTGACACCTGCTCTCAGGCAGCACCATGTTGGAAGGACATGTTCAATGTG 471
QY 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
DB 472 AACGTGCTGGCCCTCAGCATCTGCACCGGAAGCCTACCATGTCATGAAGAGCGGAAT 531
QY 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
DB 532 GTGGAGCATGGGCATCATATTAACTCAATAGCATGTCTGGCCACCGAGTGTACCCCTG 591
QY 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
DB 592 TCTGTGACCACTTCTATAGTGCCACCAAGTATGCCGTCACTGCGCTGACAGAGGACTG 651
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DB 652 AGGCAAGAGCTTCTGGGAGCGCCAGACCCACATCCGAGGCACGTGCTCTCCAGGTGG 711
QY 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaThr 220
DB 712 GTGGAGACCAATTCCCTTCAAACTCCACGACAGGACCTTGAGAGCGCAGTCCAC 771
QY 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
DB 772 TATGACAAATGAAGTGTCTCAAAACCGAGGATGTGGCGGAGGCTGTTATCTACGCTCTC 831

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QY 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
DB 832 AGCACCCCGCACATCCAGATTGGAGACATCCAGATGAGGCCACGACGAGTGAC 891

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XX
DT 11-AUG-2003 (first entry)
XX
DE Human secreted polypeptide PRO1774-encoding cDNA, SEQ ID NO:377.
XX
KW Human; PRO; secreted protein; transmembrane protein;
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;
KW chondrocyte; proliferation; differentiation; cartilage disorder;
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;
KW liver; drug screening; transgenic animal; genetic analysis;
KW antiarthritic; vulnery; gene therapy; gene; ss.
XX
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XX
PN US2003027264-A1.
XX
PD 06-FEB-2003.
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Alignment Scores:
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 Score: 1337.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 7
 Length: 1505
 Matches: 260
 Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-10-063-735-128 (1-260) x ACC89538 (1-1505)

QY 1 MetAlaArgProGlyMetGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSer 20

Db	112	ATGCCAGCCCGCCGATGGAGCGTGGCGGACCGGCTGGGCTGGTACGGGGCCCTCG	171	XX	18-SEP-1997;	97US-0059263P.
Qy	21	GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly	40	PR	18-SEP-1997;	97US-0059266P.
Db	172	GGGGGATCGCGCGCGCGTGGCCCGGCGCTGGTCCAGCAGGAGACTGAAGTGGTGGGC	231	PR	17-OCT-1997;	97US-0062250P.
Qy	41	CysAlaArgThrValGlyAsnIleGluLeuAlaGluCysLysSerAlaGlyTyr	60	PR	21-OCT-1997;	97US-0063486P.
Db	232	TGCGCCCGCAGTGTGGCAACATCGAGAGCTGGCTGTAATGTAAGAGTGCAGGCTAC	291	PR	24-OCT-1997;	97US-0063120P.
Qy	61	ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet	80	PR	28-OCT-1997;	97US-0063540P.
Db	292	CCCGGAGTTTGATCCCTACAGATGTGACCTATCAATGAAGAGCATCTCTCCATG	351	PR	28-OCT-1997;	97US-0063544P.
Qy	81	PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu	100	PR	29-OCT-1997;	97US-0063734P.
Db	352	TTCTCAGCTATCCGTCTTCAGCACAGCGGTGTAGACATCTGCATCAACATGCTGGCTTG	411	PR	31-OCT-1997;	97US-0063870P.
Qy	101	AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnVal	120	PR	31-OCT-1997;	97US-0064103P.
Db	412	GCCCGGCGTGCACCCCTGCTCTCAGGCGACCCAGTGGTGGAGGACATGTTCAATGTG	471	PR	13-NOV-1997;	97US-0065311P.
Qy	121	AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn	140	PR	21-NOV-1997;	97US-0066120P.
Db	472	AACGTGCTGGCCCTCAGCATCTGCACCGGAGACCTACCACTCCATGAAGAGCGGAT	531	PR	24-NOV-1997;	97US-0066466P.
Qy	141	ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu	160	PR	11-DEC-1997;	97US-0066772P.
Db	532	GTGGACGATGGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTG	591	PR	12-DEC-1997;	97US-0069335P.
Qy	161	SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu	180	PR	17-DEC-1997;	97US-0069425P.
Db	592	TCTGTGACCCACTTCTATAGTGCCACCAAGATGCCGTCATCGGCTCAGAGAGGACTG	651	PR	18-DEC-1997;	97US-0069870P.
Qy	181	ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal	200	PR	10-MAR-1998;	97US-0074501P.
Db	652	AGCAAGAGCTTCGGAGGCGCCAGACCCACATCCGAGCCAGTGCATCTCTCCAGTGTG	711	PR	11-MAR-1998;	98US-0077632P.
Qy	201	ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThr	220	PR	11-MAR-1998;	98US-0077649P.
Db	712	GTGGAGACACAATTCGCCCTTCAAACTCCACGACAGGACCCCTGAGAGGCGAGCTGCCACC	771	PR	20-MAR-1998;	98US-0078866P.
Qy	221	TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu	240	PR	27-MAR-1998;	98US-0079664P.
Db	772	TATGAGCAAAATGAAGTGTCTAAACCCGAGGATGTGGCCGAGCTGTTATCTACGTCCTC	831	PR	27-MAR-1998;	98US-0079786P.
Qy	241	SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr	260	PR	31-MAR-1998;	98US-0080107P.
Db	832	AGCACCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCCCCGAGCGGTGACC	891	PR	31-MAR-1998;	98US-0080194P.

RESULT 14
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ID ACA98329 standard; cDNA; 1505 BP.
XX
AC ACA98329;
XX
DT 25-JUL-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO1774 cDNA.
XX
KW Human; secreted and transmembrane protein; PRO; transgenic animal;
KW knockout; chromosome identification; tissue typing; tumour;
KW chondrocyte proliferation; chondrocyte differentiation;
KW tumor necrosis factor-alpha release stimulator; gene; ss.
XX
OS Homo sapiens.
XX
PN US2003036144-A1.
XX
PD 20-FEB-2003.
XX
PF 01-JUL-2002; 2002US-00187601.


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Qy 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
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Qy 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
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Qy 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
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Db 712 GTGGAGACACAATTGCGCTTCAAACTCCAGACAGGACCCCTGAGAAGGCAGCTGCCACC 771
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XX proliferation; differentiation; chondrocyte cell; TNF-alpha;
XX tumour necrosis factor-alpha; gene therapy.
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PR 24-JUN-1998; 98US-0090461P.
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PR 24-JUN-1998; 98US-0090540P.
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Score: 1337.00          Matches: 260
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 100.00%      Indels: 0
DB: 7                      Gaps: 0

US-10-063-735-128 (1-260) x ACA93971 (1-1505)

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QY 61 ProGlyThrLeuIleProTyrArgCysAspIleuSerAsnGluGluAspIleuSerMet 80
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QY 121 AsnValIleuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
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QY 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
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QY 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
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QY 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
Db 652 AGGCAAGAGCTTCGGAGGCGCCAGACCCACATCCGAGCCACGTGCATCTCTCCAGGTGTG 711
QY 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThr 220
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QY 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
Db 772 TATGAGCAAAATGAAGTGTCTCAAAACCGAGGATGTGGCCGAGGCTGTTATCTACGTCTCT 831
QY 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
Db 832 AGCACCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCCGGAGAGGTGACC 891

Search completed: September 16, 2004, 17:48:11
Job time : 364 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 16, 2004, 16:36:27 : Search time 422 Seconds

(without alignments)

3109.801 Million cell updates/sec

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Perfect score: 1337

Sequence:

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3327077 seqs, 2523723180 residues

Total number of hits satisfying chosen parameters: 6654154

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
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Database : Published Applications NA:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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ALIGNMENTS

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; Sequence 222, Application US/099711392
; Publication No. US20030134283A1
; GENERAL INFORMATION:
; APPLICANT: Pearson, David P.
; APPLICANT: Cocks, Benjamin G.
; TITLE OF INVENTION: GENES REGULATED IN DENDRITIC CELL DIFFERENTIATION
; FILE REFERENCE: PA-0029 US
; CURRENT APPLICATION NUMBER: US/09/971,392
; PRIOR FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 60/237,652
; NUMBER OF SEQ ID NOS: 260
; SOFTWARE: PERL Program
; SEQ ID NO 222
; LENGTH: 1493
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Template ID: 422389.9

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6	1337	100.0	1505	13	US-10-208-024-377	Sequence 377, App	
7	1337	100.0	1505	13	US-10-201-853-377	Sequence 377, App	
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16	1337	100.0	1505	13	US-10-176-914-377	Sequence 377, App	
17	1337	100.0	1505	13	US-10-176-915-377	Sequence 377, App	
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US-09-971-392-222

Alignment Scores:

Pred. No.: 1.83e-165 Length: 1493
Score: 1337.00 Matches: 260
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

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Db 172 GGGGGCATCG 231
Qy 41 CysAlaArgThrValGlyAsnIleGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
Db 232 TGGCGCCGCACCTGTGGGCAACATCGAGGAGTGGCTGCTGAATGTAAGAGTGCAGGCTAC 291
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Qy 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeu 100
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Db 412 GCGCGGCTGACACCGCTGCTCTCAGCGAGCAGCAGTGGTGGAGGAGCATGTTCAATGTG 471
Qy 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgSer 140
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RESULT 2

US-10-206-915-377
; Sequence 377, Application US/10206915
; Publication No. US20040029221A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zenin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C513
; CURRENT APPLICATION NUMBER: US/10/206,915
; CURRENT FILING DATE: 2002-07-26
; PRIORITY APPLICATION NUMBER: 10/052586
; PRIORITY FILING DATE: 2002-01-15
; PRIORITY APPLICATION NUMBER: 60/059263
; PRIORITY FILING DATE: 1997-09-18
; PRIORITY APPLICATION NUMBER: 60/059266
; PRIORITY FILING DATE: 1997-09-18
; PRIORITY APPLICATION NUMBER: 60/062250
; PRIORITY FILING DATE: 1997-10-17
; PRIORITY APPLICATION NUMBER: 60/063120
; PRIORITY FILING DATE: 1997-10-24
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; PRIORITY FILING DATE: 1997-10-24
; PRIORITY APPLICATION NUMBER: 60/063486
; PRIORITY FILING DATE: 1997-10-21
; PRIORITY APPLICATION NUMBER: 60/063540
; PRIORITY FILING DATE: 1997-10-28
; PRIORITY APPLICATION NUMBER: 60/063541
; PRIORITY FILING DATE: 1997-10-28
; PRIORITY APPLICATION NUMBER: 60/063544
; PRIORITY FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 377
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-206-915-377

Alignment Scores:

Pred. No.: 1.83e-165 Length: 1505
Score: 1337.00 Matches: 260
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-735-128 (1-260) x US-10-206-915-377 (1-1505)

Qy 1 MetAlaArgProGlyMetGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSer 20
Db 112 ATGCCAGGCCCGCGCATGGAGCGGTGGCGCGACCGGCTGGTGACCGGGGCGCTCG 171
Qy 21 GlyGlyLeuGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly 40
Db 172 GGGGGCATCG 231
Qy 41 CysAlaArgThrValGlyAsnIleGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
Db 232 TGGCGCCGCACCTGTGGGCAACATCGAGGAGTGGCTGCTGAATGTAAGAGTGCAGGCTAC 291
Qy 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluAlaAspIleSerMet 80
Db 292 CCGGGGACTTTGATCCCTACAGATGTGACCTATCAAAATGAAGAGGACATCTCTCCATG 351
Qy 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeu 100
Db 352 TTCTCAGTATCCGTTCTTCAGCACAGCGGTGAGACATCTGCATCAACAATGCTGGCTTG 411
Qy 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnVal 120
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QY 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
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QY 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
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; Publication No. US20040033560A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C401
; CURRENT APPLICATION NUMBER: US/10/199,670
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 377
```

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; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-199-670-377

Alignment Scores:
Pred. No.: 1,83e-165 Length: 1505
Score: 1337.00 Matches: 260
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-735-128 (1-260) x US-10-199-670-377 (1-1505)
QY 1 MetAlaArgProGlyMetGluArgTyrArgAspArgLeuAlaLeuValThrGlyAlaSer 20
Db 112 ATGCCAGGCCCGGCATGGAGCGGTGGCGGACCGGCTGGCTGGTGACGGGGGCGCTCG 171
QY 21 GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly 40
Db 172 GGGGGCATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 231
QY 41 CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
Db 232 TGGCGCCGCACTGTGGGCAACATCGAGGAGCTGGCTGCTGAATGTAAGAGTGCAGGCTAC 291
QY 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet 80
Db 292 CCCGGGACTTGTATCCCTCAGATGTGACCTATCAATGAAGAGGACATCTCTCCCATG 351
QY 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu 100
Db 352 TTCTCAGCATTCGGTTCTCAGCACGCGGTGTAGACATCTGCATCAACAATGCTGGCTTG 411
QY 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnVal 120
Db 412 GCCCGGCTGACACCCCTGCTCTCAGGCAGCACCCAGTGGTGGAGGAGCATGTTCAATGTG 471
QY 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
Db 472 AACGTGTGGCCCTCAGCATCTGCACACGGGAAGCCTACCAGTCCATGAAGGAGCGGAAT 531
QY 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
Db 532 GTGGACCATGGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTG 591
QY 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
Db 592 TCTGTGACCCACTTCTATAGTGCACCAAGTATGCCGTCACTGCGCTGCACAGAGGACTG 651
QY 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
Db 652 AGGCAAGAGTTCGGGAGGCCACAGACCCACATCCGAGCCACGTGCATCTCTCCAGGTGTG 711
QY 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaThr 220
Db 712 GTGGAGACACAAATTCGCTTCAAACTCCACGACAGGACCGCTGGAAGGCGAGTGGCCACC 771
QY 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
Db 772 TATGAGCAAAATGAAGTGTCTCAAAACCGAGGATGTGGCCGAGGCTGTATCTACGTCTC 831
QY 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
Db 832 AGCACCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCCGCCAGGAGCGGTGACC 891

RESULT 4
US-10-858-377
; Sequence 377, Application US/10201858
; Publication No. US20040038337A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
```

:	APPLICANT:	Chen,Jian
:	APPLICANT:	Desnoyers,Luc
:	APPLICANT:	Goddard,Audrey
:	APPLICANT:	Godowski,Paul J.
:	APPLICANT:	Gurney,Austin L.
:	APPLICANT:	Pan,James
:	APPLICANT:	Smith,Victoria
:	APPLICANT:	Watanabe,Colin K.
:	APPLICANT:	Wood,William I.
:	APPLICANT:	Zhang,Zemin
:	TITLE OF INVENTION:	SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
:	FILE REFERENCE:	E3430RIC464
:	CURRENT APPLICATION NUMBER:	US/10/201,858
:	CURRENT FILING DATE:	2002-07-23
:	PRIOR APPLICATION NUMBER:	10/052586
:	PRIOR FILING DATE:	2002-01-15
:	PRIOR APPLICATION NUMBER:	60/059263
:	PRIOR FILING DATE:	1997-09-18
:	PRIOR APPLICATION NUMBER:	60/059266
:	PRIOR FILING DATE:	1997-09-18
:	PRIOR APPLICATION NUMBER:	60/062250
:	PRIOR FILING DATE:	1997-10-17
:	PRIOR APPLICATION NUMBER:	60/063120
:	PRIOR FILING DATE:	1997-10-24
:	PRIOR APPLICATION NUMBER:	60/063121
:	PRIOR FILING DATE:	1997-10-24
:	PRIOR APPLICATION NUMBER:	60/063486
:	PRIOR FILING DATE:	1997-10-21
:	PRIOR APPLICATION NUMBER:	60/063540
:	PRIOR FILING DATE:	1997-10-28
:	PRIOR APPLICATION NUMBER:	60/063541
:	PRIOR FILING DATE:	1997-10-28
:	PRIOR APPLICATION NUMBER:	60/063544
:	PRIOR FILING DATE:	1997-10-28
:	Prior Application data removed - See File Wrapper or PALM.	
:	NUMBER OF SEQ ID NOS:	612
:	SEQ ID NO 377	
:	LENGTH:	1505
:	TYPE:	DNA
:	ORGANISM:	Homo Sapien
:	US-10-201-858-377	
:	Alignment Scores:	
:	Pred. No.:	1.83e-165
:	Score:	1337.00
:	Length:	1505
:	Percent Similarity:	100.00%
:	Conservative:	0
:	Best Local Similarity:	100.00%
:	Mismatches:	0
:	Query Match:	100.00%
:	Indels:	0
:	Gaps:	0
:	DB:	13
:	US-10-063-735-128 (1-260) x US-10-201-858-377 (1-1505)	
:QY	1	MetaAlaArgProGlyMetGluArgTrpArgAspArgLeuAlaValThrGlyAlaSer 20
:Db	112	ATGGCCAGCCCGCATGGAGTGGCGGCACCGGTGGCGCTGGTGTCGACGGGGCCTCG 171
:QY	21	GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly 40
:Db	172	GGGGGCATCGGCCGGCCGTGGCCCGGCCCTGTGTCAGACAGGGACTGAAGGTGGTGGG 231
:QY	41	CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCybsLysSerAlaGlyTyr 60
:Db	232	TGCGCCGCACATGTGGCAACATCGAGAGCTGGCTCTCTAATTAAAGTAGTGCAGGCTAC 291
:QY	61	ProGlyThrLeuIleProTyArgCysAspLeuSerAsnGluGluAspIleLeuSerMet 80
:Db	292	CCCGGGACTTTGATCCCTACAGATGTGACCTATCAAATGAAGAGGACATCCTCTCCATG 351
:QY	81	PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeu 100
:Db	352	TTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACAATGCTGCTTG 411

; Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 377

; LENGTH: 1505

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-205-890-377

Alignment Scores:

Pred. No.: 1.83e-165 Length: 1505
Score: 1337.00 Matches: 260
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-735-128 (1-260) x US-10-205-890-377 (1-1505)

```
Qy 1 MetAlaArgProGlyMetGluAtrGTrpArgAspArgLeuAlaLeuValThrGlyAlaSer 20
Db 112 ATGCCAGGCCCGCATGGAGCGGTGGCGACCGCGCTGGCGTGGTGGAGGGGGCCCTCG 171
Qy 21 GlyGlyLeuGlyAlaAlaValAlaAraAlaLeuValGlnGlnGlyLeuLysValValGly 40
Db 172 GGGGGCATCGCGCGCGCGTGGCGCGCGTGGTCCAGCAGGAGCTGAAGGTGGTGGGC 231
Qy 41 CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
Db 232 TGGCGCCGCACTGTGGGCAACATCGAGGAGTGGCTGCTGAATGAAGAGTGCAGGGCTAC 291
Qy 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet 80
Db 292 CCGGGGACTTTGATCCCTCAGATGACCTATCAATGAAGAGGACATCTCTCCCATG 351
Qy 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu 100
Db 352 TTCTCAGCTATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACATGCTGGCTTG 411
Qy 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnVal 120
Db 412 GCCCGGCTGACACCTGCTCTCAGGCGAGCACCAGTGGTGGAAAGGACATGTTCAATGT 471
Qy 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
Db 472 AACGTGTCGCCCTCAGCATCTGCACGCGGAACCTACCATGCTCAATGAAGGCGGAAT 531
Qy 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
Db 532 GTGGACCATGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTG 591
Qy 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
Db 592 TCTGTGACCACTTCTATAGTGCACCAAGTATGCCGTCACTGCCGTGACAGAGGACTG 651
Qy 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
Db 652 AGGCAAGAGCTTCGGGAGGCCACACCATCCGAGCCAGTGCTCATCTCTCCAGGTGTG 711
Qy 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThr 220
Db 712 GTGGAGACACAAATTCGCTTCAAACTCCACGACAAGGACCTCGAGAGGCGAGCTGCCACC 771
Qy 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
Db 772 TATGAGCAAAATGAAGTGTCTCAAAACCCGAGGATGTGGCCGAGGCTGTATCTACGCTCCT 831
Qy 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
Db 832 AGCACCCCGCACATCTCAGATTGGAGACATCCAGATGAGGCCCGCCGAGGAGGTGACC 891
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RESULT 6

US-10-208-024-377

; Sequence 377, Application US/10208024

; Publication No. US20040048335A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: F3430R1C538

; CURRENT APPLICATION NUMBER: US/10/208,024

; CURRENT FILING DATE: 2002-07-29

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063120

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063121

; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486

; PRIOR FILING DATE: 1997-10-21

; PRIOR APPLICATION NUMBER: 60/063540

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063541

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/063544

; PRIOR FILING DATE: 1997-10-28

; Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 377

; LENGTH: 1505

; TYPE: DNA

; ORGANISM: Homo Sapien

US-10-208-024-377

Alignment Scores:

Pred. No.: 1.83e-165 Length: 1505
Score: 1337.00 Matches: 260
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-735-128 (1-260) x US-10-208-024-377 (1-1505)

```
Qy 1 MetAlaArgProGlyMetGluAtrGTrpArgAspArgLeuAlaLeuValThrGlyAlaSer 20
Db 112 ATGCCAGGCCCGCATGGAGCGGTGGCGACCGCGCTGGCGTGGTGGAGGGGGCCCTCG 171
Qy 21 GlyGlyLeuGlyAlaAlaValAlaAraAlaLeuValGlnGlnGlyLeuLysValValGly 40
Db 172 GGGGGCATCGCGCGCGCGTGGCGCGCGTGGTCCAGCAGGAGCTGAAGGTGGTGGGC 231
Qy 41 CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
Db 232 TGGCGCCGCACTGTGGGCAACATCGAGGAGTGGCTGCTGAATGAAGAGTGCAGGGCTAC 291
Qy 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet 80
Db 292 CCGGGGACTTTGATCCCTCAGATGACCTATCAATGAAGAGGACATCTCTCCCATG 351
Qy 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu 100
```

```
Db 352 TTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACAATGCTGGCTTG 411
Qy 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnVal 120
Db 412 GCCCGGCGCTGACACCTCTCTCAGGACAGCCAGTGGTGGAGAGACATGTTCAATGTG 471
Qy 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
Db 472 AACGTGCTGGCCCTCAGCATCTGCACCGGAAGCCTACCACTCATGAAGAGCGGAAT 531
Qy 141 ValAspAspGlyHisIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
Db 532 GTGACGATGGCGACATCAATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTG 591
Qy 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
Db 592 TCTGTGACCCCACTTCTATAGTGCCCAAGATATGCCGTCACTGGCGCTGACAGAGGACTG 651
Qy 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
Db 652 AGGCAAGAGCTTCGGAGGCCCGACACCATCCGAGGCAGTGCATCTCTCCAGGTGTG 711
Qy 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThr 220
Db 712 GTGGAGACACAATTCGCCCTTCAAACTCCACGACAAGGACCTGAGAAGGCGAGCTGCCACC 771
Qy 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
Db 772 TATGAGCAAAATGAAGTGTCTCAAAACCCGAGATGTGGCCGAGGTGTTATCTACGTCCTC 831
Qy 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
Db 832 AGCACCCCGCACATCCAGATTGGAGACATCCAGATGAGGCCCCACGAGCAGCGTGACC 891
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RESULT 7

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US-10-201-853-377
; Sequence 377, Application US/10201853
; Publication No. US20040053358A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C465
; CURRENT APPLICATION NUMBER: US/10/201,853
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
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; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 377
```

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; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-201-853-377
```

Alignment Scores:

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Pred. No.: 1,83e-165 Length: 1505
Score: 1337.00 Matches: 260
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
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US-10-063-735-128 (1-260) x US-10-201-853-377 (1-1505)

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Qy 1 MetAlaArgProGlyMetGluArgTyrArgAspArgLeuAlaLeuValThrGlyAlaSer 20
Db 112 ATGCCACAGGCCCGCATGGAGCGGTGGCGACCGGCTGGCGCTGGTACGGGGGCGCTCG 171
Qy 21 GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly 40
Db 172 GGGGGCATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 231
Qy 41 CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
Db 232 TGCSCCGGCATCTGGGCGACATCGAGAGCTGGCTGCTGAATGTAAAGTGCAGGCTAC 291
Qy 61 ProGlyThrIleuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet 80
Db 292 CCCGGGACCTTGTATCCCGCTACAGATGTGACCTATCAATGAAGAGGACATCTCTCCATG 351
Qy 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu 100
Db 352 TTCTCAGCTATCCCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACAATGCTGGCTTG 411
Qy 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrLysAspMetPheAsnVal 120
Db 412 GCCCGGCGCTGACACCTCTCTCAGGACAGCACCACTGGTGGAGAGACATGTTCAATGTG 471
Qy 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
Db 472 AACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTACCACTCATGAAGAGCGGAAT 531
Qy 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
Db 532 GTGACGATGGCGACATCAATTAACATCAATAGCATGTCTGGCCACCGAGTGTACCCCTG 591
Qy 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
Db 592 TCTGTGACCCCACTTCTATAGTGCCACCAAGTATGCCGTCACTGGCGCTGACAGAGGACTG 651
Qy 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
Db 652 AGGCAAGAGCTTCGGAGGCCCGACACCATCCAGAGCCTACCACTCATGAAGAGCGGAAT 711
Qy 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThr 220
Db 712 GTGGAGACACAATTCGCCCTTCAAACTCCACGACAAGGACCTGAGAAGGCGAGCTGCCACC 771
Qy 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
Db 772 TATGAGCAAAATGAAGTGTCTCAAAACCCGAGATGTGGCCGAGGTGTTATCTACGTCCTC 831
Qy 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
Db 832 AGCACCCCGCACATCCAGATTGGAGATTCAGATGAGGCCCCACGAGCAGCGTGACC 891
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RESULT 8
US-10-063-745-127
; Sequence 127, Application US/10063745
; Publication No. US20040058411A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,745
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 127
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-745-127

Alignment Scores:
Pred. No.: 1.83e-165      Length: 1505
Score: 1337.00           Matches: 260
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%           Indels: 0
DB: 13                     Gaps: 0

US-10-063-735-128 (1-260) x US-10-063-745-127 (1-1505)

Qy 1 MetAlaArgProGlyMetGluAtrGTPArgAspArgLeuAlaLeuValThrGlyAlaSer 20
Db 112 ATGCCAGGCGCGCATGGAGCGGTGGCGGACCGGCTGGCGCTGGTGAAGGGGCGCTCG 171
Qy 21 GlyGlyIleGlyAlaAlaValAlaAraArgAlaLeuValGlnGlnGlyLeuLysValValGly 40
Db 172 GGGGGCATCGGCGCGCGTGGCCCGGCGCTGGTCCAGCAGGACTGTAAGTGGTGGGC 231
Qy 41 CysAlaArgThrValGlyAsnIleGluLeuAlaGluCysLysSerAlaGlyTyr 60
Db 232 TGCGCCCGCACTGTGGGCAACATCGAGAGCTGGCTGCTGAATGAAGAGTGCAGGCTAC 291
Qy 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluAspIleLeuSerMet 80
Db 292 CCCGGGACTTTGATCCCTACAGATGTGACCTATCAATGAAGAGGACATCTCTCCATG 351
Qy 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeu 100
Db 352 TTCTCAGTATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACAATGCTGGCTTG 411
Qy 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnVal 120
Db 412 GCCCGGCTGACACCTGCTCTCAGGAGCAGCACCAGTGGTGGAGGACATGTTCAATGTG 471
Qy 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
Db 472 AACGTGCTGGCCCTCAGCATCTGCACACGGGAAGCCTACCATGTCATGAAGAGCGGAAT 531
Qy 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
Db 532 GTGACCGATGGGCACATCAATTAACATCAATAGCATGCTGGCCACCGAGTGTACCCCTG 591
Qy 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
Db 592 TCTGTGACCCACTTCTATAGTGCCACCAAGTATGCCGCTACTCGCTGACAGAGGGACTG 651

RESULT 9
US-10-063-512-127
; Sequence 127, Application US/10063512
; Publication No. US20030018183A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 127
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-512-127

Alignment Scores:
Pred. No.: 1.83e-165      Length: 1505
Score: 1337.00           Matches: 260
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%           Indels: 0
DB: 13                     Gaps: 0

US-10-063-735-128 (1-260) x US-10-063-512-127 (1-1505)

Qy 1 MetAlaArgProGlyMetGluAtrGTPArgAspArgLeuAlaLeuValThrGlyAlaSer 20
Db 112 ATGCCAGGCGCGCATGGAGCGGTGGCGGACCGGCTGGCGCTGGTGAAGGGGCGCTCG 171
Qy 21 GlyGlyIleGlyAlaAlaValAlaAraArgAlaLeuValGlnGlnGlyLeuLysValValGly 40
Db 172 GGGGGCATCGGCGCGCGTGGCCCGGCGCTGGTCCAGCAGGACTGTAAGTGGTGGGC 231
Qy 41 CysAlaArgThrValGlyAsnIleGluLeuAlaGluCysLysSerAlaGlyTyr 60
Db 232 TGCGCCCGCACTGTGGGCAACATCGAGAGCTGGCTGCTGAATGAAGAGTGCAGGCTAC 291
Qy 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluAspIleLeuSerMet 80
Db 292 CCCGGGACTTTGATCCCTACAGATGTGACCTATCAATGAAGAGGACATCTCTCCATG 351
Qy 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeu 100
Db 352 TTCTCAGTATCCGTTCTCAGCAGCGGTGTAGACATCTGCATCAACAATGCTGGCTTG 411
```

Qy 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnVal 120
 Db 412 GCCCGGCTGACACCCCTGCTCTCAGGAGCAGCAGGAGTGGTGAAGGACATGTTCAATGTG 471
 Qy 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTrpGlnSerMetLysGluArgAsn 140
 Db 472 AACGTGTGGCCCTCAGCATCTGCACAGGGAAGCCTACCAAGTCCATGAAGAGCGGAT 531
 Qy 141 ValAspAspGlyHisIleLeuAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
 Db 532 GTGGACGATGGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTATCCCTG 591
 Qy 161 SerValThrHisPheThrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
 Db 592 TCTGTGACCCACTTCTATAGTGGCCACCCAGTATGCGTCACTGCGTGCAGAGGAGCTG 651
 Qy 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
 Db 652 AGCAAGAGCTTCGGGAGGCCAGACCCACATCCGAGCCAGTGCATCTCTCCAGGTGTG 711
 Qy 201 ValGlnThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThr 220
 Db 712 GTGGAGACACAATTCGCGCTTCAAACTCCACAGGAGCCCTGAGAGGCGAGCTGCCACC 771
 Qy 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
 Db 772 TATGAGCAATGAAGTGTCTCAAAACCCGAGGATGTGGCCGAGGCTGTATCTAGTCTCTC 831
 Qy 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
 Db 832 AGCACCCCGCACATCCAGATTGGAGACATCCAGATGAGGCCACCGAGCGAGTGTACC 891

RESULT 10

US-10-063-513-127
 ; Sequence 127, Application US/10063513
 ; Publication No. US20030018172A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3230R1C1
 ; CURRENT APPLICATION NUMBER: US/10/063,513
 ; PRIORITY FILING DATE: 2002-05-01
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 127
 ; LENGTH: 1505
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 US-10-063-513-127

Alignment Scores:

Pred. No.: 1,83e-165 Length: 1505
 Score: 1337.00 Matches: 260
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-10-063-735-128 (1-260) x US-10-063-513-127 (1-1505)

Qy 1 MetAlaArgProGlyMetGluArgTrpArgAspArgLeuAlaLeuValThrGlyAlaSer 20
 Db 112 ATGGCCAGGCGCGCATGAGCGGTGGCGGACCGGCTGGTACGCGGCGCTCG 171

Qy 21 GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly 40
 Db 172 GGGGCGCATCGCGCGCGCGCGTGGCCCGGCGCTGTGTCCAGCAGGAGCTGAAGGTGTGGGC 231
 Qy 41 CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
 Db 232 TGGCCCGGCATCTGTGGCAACATCGAGGAGCTGCTGCTGAATGTAAGAGTGCAGGCTAC 291
 Qy 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet 80
 Db 292 CCCGGGACTTTTGATCCCTTACAGATGTGACCTATCAAAATGAAGAGGACATCTCTCCATG 351
 Qy 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu 100
 Db 352 TTTCTAGCTATTCCTGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACATGCTGGCTTG 411
 Qy 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnVal 120
 Db 412 GCCCGGCTGACACCCCTGCTCTCAGGAGCAGCAGGAGTGGTGGAAAGGACATGTTCAATGTG 471
 Qy 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTrpGlnSerMetLysGluArgAsn 140
 Db 472 AACGTGTGGCCCTCAGCATCTGCACAGGGAAGCCTACCAAGTCCATGAAGAGCGGAT 531
 Qy 141 ValAspAspGlyHisIleLeuAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
 Db 532 GTGGACGATGGGCACATCATTAACATCAATAGCATGTCTGGCCACCGAGTGTATCCCTG 591
 Qy 161 SerValThrHisPheThrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
 Db 592 TCTGTGACCCACTTCTATAGTGGCCACCAAGTATGCCGTCACTGCGTGCAGAGGAGCTG 651
 Qy 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
 Db 652 AGCAAGAGCTTCGGGAGGCCAGACCCACATCCGAGCCAGTGCATCTCTCCAGGTGTG 711
 Qy 201 ValGlnThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThr 220
 Db 712 GTGGAGACACAATTCGCGCTTCAAACTCCACAGGAGCCCTGAGAGGCGAGCTGCCACC 771
 Qy 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
 Db 772 TATGAGCAATGAAGTGTCTCAAAACCCGAGGATGTGGCCGAGGCTGTATCTAGTCTCTC 831
 Qy 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
 Db 832 AGCACCCCGCACATCCAGATTGGAGACATCCAGATGAGGCCACCGAGCGAGTGTACC 891

RESULT 11

US-10-063-569-127
 ; Sequence 127, Application US/10063569
 ; Publication No. US20030018168A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, Christopher J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3230R1C1
 ; CURRENT APPLICATION NUMBER: US/10/063,569
 ; PRIORITY FILING DATE: 2002-05-02
 ; Prior Application removed - See File Wrapper or Palm
 ; NUMBER OF SEQ ID NOS: 170
 ; SEQ ID NO 127
 ; LENGTH: 1505
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien

US-10-063-569-127

Alignment Scores:
Pred. No.: 1.83e-165 Length: 1505
Score: 1337.00 Matches: 260
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-735-128 (1-260) x US-10-063-569-127 (1-1505)

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QY 1 MetAlaArgProGlyMetGluAArgTyrArgAspArgLeuAlaLeuValThrGlyAlaSer 20
DB 112 ATGCCAGGCCCGCATGGAGCGGTGGCGGACCGGCTGGCTGGTGCAGCGGGGCTCG 171
QY 21 GlyGlyLeuGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuValValGly 40
DB 172 GGGGGCATCGCGCGCGCGGTGGCGCGGCTGGTCCAGCAGGAGCTGAAGGTGGTGGC 231
QY 41 CysAlaArgThrValGlyAsnIleGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
DB 232 TGGCGCGCATCTGGGCAACATCGAGAGCTGGCTGCTGAATGAAGAGTGCAGGCTAC 291
QY 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet 80
DB 292 CCGGGGACTTGTATCCCTACAGATGTGACCTATCAAAATGAAGAGGACATCTCTCCATG 351
QY 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeu 100
DB 352 TTCTCAGCTATCCGCTTCTCAGCAGCGGTGTAGACATCTGCATCAACAATGCTGGCTG 411
QY 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrIleAspMetPheAsnVal 120
DB 412 GCCCGGCTTACACCTCTCTCAGGAGCAGCAGTGGTGGAGAGGACATGTTCAATGTG 471
QY 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaThrGlnSerMetLysGluArgAsn 140
DB 472 AACGTGCTGGCCCTCAGCATCTGCACACGGGAGCCTACCACTCCATGAAGAGCGGAAT 531
QY 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
DB 532 GTGGAGCATGGGCACATCAATTAACATAGCATGTCTGGCCACCGAGTGTACCCCTG 591
QY 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
DB 592 TCTGTGACCCACTTCTATAGTGGCCACCAAGTATGCGCTCATCGCTGCAGAGGACTG 651
QY 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
DB 652 AGCAGAGCTTGGGAGGCGCCAGACCAATCCGAGCCAGTGCATCTCTCCAGGTGTG 711
QY 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThr 220
DB 712 GTGGAGACACAATTCGCTTCAAACTCCACGACAAAGGACCTGAGAGGCGAGCTGCCACC 771
QY 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
DB 772 TATGAGCAATGAAAGTGTCTCAAAACCCGAGGATGTGGCCGAGGCTGTATCTACGCTCT 831
QY 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
DB 832 AGCACCCCGCACATCCAGATTTGGAGACATCCAGATGAGGCCCGGAGGAGTGAACC 891
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RESULT 12

US-10-063-551-127
; Sequence 127, Application US/10063551
; Publication No. US20020183494A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,551
; PRIOR FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 127
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-551-127

Alignment Scores:
Pred. No.: 1.83e-165 Length: 1505
Score: 1337.00 Matches: 260
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-735-128 (1-260) x US-10-063-551-127 (1-1505)

```
QY 1 MetAlaArgProGlyMetGluAArgTyrArgAspArgLeuAlaLeuValThrGlyAlaSer 20
DB 112 ATGCCAGGCCCGCATGGAGCGGTGGCGGACCGGCTGGCTGGTGCAGCGGGGCTCG 171
QY 21 GlyGlyLeuGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuValValGly 40
DB 172 GGGGGCATCGCGCGCGCGGTGGCGCGGCTGGTCCAGCAGGAGCTGAAGGTGGTGGC 231
QY 41 CysAlaArgThrValGlyAsnIleGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
DB 232 TGGCGGCTTACACCTCTCTCAGGAGCAGCAGTGGTGGAGAGGACATGTTCAATGTG 291
QY 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGluGluAspIleLeuSerMet 80
DB 292 CCGGGGACTTGTATCCCTACAGATGTGACCTATCAAAATGAAGAGGACATCTCTCCATG 351
QY 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAlaGlyLeu 100
DB 352 TTCTCAGCTATCCGCTTCTCAGCAGCGGTGTAGACATCTGCATCAACAATGCTGGCTG 411
QY 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTyrIleAspMetPheAsnVal 120
DB 412 GCCCGGCTTACACCTCTCTCAGGAGCAGCAGTGGTGGAGAGGACATGTTCAATGTG 471
QY 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaThrGlnSerMetLysGluArgAsn 140
DB 472 AACGTGCTGGCCCTCAGCATCTGCACACGGGAGCCTACCACTCCATGAAGAGCGGAAT 531
QY 141 ValAspAspGlyHisIleIleAsnIleAsnSerMetSerGlyHisArgValLeuProLeu 160
DB 532 GTGGAGCATGGGCACATCAATTAACATAGCATGTCTGGCCACCGAGTGTACCCCTG 591
QY 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
DB 592 TCTGTGACCCACTTCTATAGTGGCCACCAAGTATGCGCTCATCGCTGCAGAGGACTG 651
QY 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
DB 652 AGCAGAGCTTGGGAGGCGCCAGACCAATCCGAGCCAGTGCATCTCTCCAGGTGTG 711
QY 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThr 220
DB 712 GTGGAGACACAATTCGCTTCAAACTCCACGACAAAGGACCTGAGAGGCGAGCTGCCACC 771
QY 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
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Db 772 TATGAGCAATGAAGTCTCTCAACCCGAGGATGTGGCCGAGGTGTATCTAGTCTC 831
Qy 241 SerThrProIaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
Db 832 AGCACCCCGCACACATCCAGATTGGAGATCCAGATCAGATGAGGCCACCGAGCGGTGACC 891
RESULT 13
US-10-174-581-377
; Sequence 377, Application US/10174581
; Publication No. US20030017540A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C41
; CURRENT APPLICATION NUMBER: US/10174, 581
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063564
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063734
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 60/063870
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066120
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/066466
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/066772
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/069335
; PRIOR FILING DATE: 1997-12-11
; PRIOR APPLICATION NUMBER: 60/069425
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: 60/069870
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/068017
; PRIOR FILING DATE: 1997-12-18
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/078886
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/078939
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079664
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/079786
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/080107
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080194
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/080327
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/080333
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: 60/081049
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081070
; PRIOR FILING DATE: 1998-04-08
; PRIOR APPLICATION NUMBER: 60/081195
; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081838
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082568
; PRIOR FILING DATE: 1998-04-21
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; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/082704
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/082797
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/083322
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; PRIOR APPLICATION NUMBER: 60/083499
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; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086023
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/086486
; PRIOR FILING DATE: 1998-05-22

; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 377
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-483-377

Alignment Scores:
Pred. No.: 1.83e-165 Length: 1505
Score: 1337.00 Matches: 260
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-735-128 (1-260) x US-10-176-483-377 (1-1505)

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Qy 1 MetAlaArgProGlyMetGluArgTTrpArgAspArgLeuAlaLeuValThrGlyAlaSer 20
Db 112 ATGCCAGGCGCGCATGGAGCGGTGGCGCGACCGCGTGGCGTGGTGGACGGGGGCGCTCG 171
Qy 21 GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly 40
Db 172 GGGGGCATCGCGCGCGCGTGGCGCGCCCTGGTCCAGCAGGAGCTGAAGGTGGTGGGC 231
Qy 41 CysAlaArgThrValGlyAsnIleGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
Db 232 TGCGCCCGCATCTGGCGCAACATCAGAGAGCTGGCTGCTGAATGTAAGTGCAGGCTAC 291
Qy 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGlnGluAspIleLeuSerMet 80
Db 292 CCGGGGACTTTGATCCCTACAGATGTGACCTATCAATGAAGAGGACATCCTCTCCATG 351
Qy 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu 100
Db 352 TTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACATGCTGGCTG 411
Qy 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnVal 120
Db 412 GCCCGGCGCTGACACCCCTCTCTCAGGACAGCACCAGTGGTTGGAAGGACATGTTCAATGTG 471
Qy 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
Db 472 AACGTGCTGGCGCTCAGCATCTGCACAGGAGCGCTACCAAGTCCATGAAGAGCGGAAT 531
Qy 141 ValAspAspGlyHisIleAlaPheLysLeuHisAspLysAspProGlyLysAlaAlaThr 160
Db 532 GTGGAGCATGGGCACATCAATCAATAGCATGTCTGSCCACCAGTGTACCCCTG 591
Qy 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
Db 592 TCTGTGACCCACTTCTATAGTCCACCAAGATGATGCCGTCACTGGCGTGCACAGAGGACTG 651
Qy 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
Db 652 AGGCAAGAGCTTGGGAGGCCACACCCATCCAGCCAGCATCTCTCCAGGTGTG 711
Qy 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGlyLysAlaAlaThr 220
Db 712 GTGGAGACACAATTCGCCTTCAAACTCCACCAAGGACCTTGAGAGGCGAGCTGCCACC 771
Qy 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
Db 772 TATGAGCAAAATGAAGTGTCTCAAAACCCGAGATGTGGCCGAGGTGTTATCTAGCTCTC 831
Qy 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
Db 832 AGCACCCCGCACACATCCAGNTTGGAGACATCCAGATGAGGCCACCGAGCAGGTGACC 891
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RESULT 15

US-10-176-749-377

; Sequence 377, Application US/10176749
; Publication No. US20030017542A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Deanovers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/10/176,749
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 377
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-749-377

Alignment Scores:
Pred. No.: 1.83e-165 Length: 1505
Score: 1337.00 Matches: 260
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-10-063-735-128 (1-260) x US-10-176-749-377 (1-1505)

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Qy 1 MetAlaArgProGlyMetGluArgTTrpArgAspArgLeuAlaLeuValThrGlyAlaSer 20
Db 112 ATGCCAGGCGCGCATGGAGCGGTGGCGCGACCGGTGGCGTGGTGGACGGGGGCGCTCG 171
Qy 21 GlyGlyIleGlyAlaAlaValAlaArgAlaLeuValGlnGlnGlyLeuLysValValGly 40
Db 172 GGGGGCATCGCGCGCGCGTGGCGCGCCCTGGTCCAGCAGGAGCTGAAGGTGGTGGGC 231
Qy 41 CysAlaArgThrValGlyAsnIleGluGluLeuAlaAlaGluCysLysSerAlaGlyTyr 60
Db 232 TGCGCCCGCATCTGGCGCAACATCAGAGAGCTGGCTGCTGAATGTAAGAGTGCAGGCTAC 291
Qy 61 ProGlyThrLeuIleProTyrArgCysAspLeuSerAsnGlnGluAspIleLeuSerMet 80
Db 292 CCGGGGACTTTGATCCCTACAGATGTGACCTATCAATGAAGAGGACATCCTCTCCATG 351
Qy 81 PheSerAlaIleArgSerGlnHisSerGlyValAspIleCysIleAsnAsnAlaGlyLeu 100
Db 352 TTCTCAGCTATCCGTTCTCAGCACAGCGGTGTAGACATCTGCATCAACATGCTGGCTG 411
Qy 101 AlaArgProAspThrLeuLeuSerGlySerThrSerGlyTrpLysAspMetPheAsnVal 120
Db 412 GCCCGGCGCTGACACCCCTCTCTCAGGACAGCACCAGTGGTTGGAAGGACATGTTCAATGTG 471
Qy 121 AsnValLeuAlaLeuSerIleCysThrArgGluAlaTyrGlnSerMetLysGluArgAsn 140
Db 472 AACGTGCTGGCGCTCAGCATCTGCACAGGAGCGCTACCAAGTCCATGAAGAGCGGAAT 531
Qy 141 ValAspAspGlyHisIleAlaPheLysLeuHisAsnSerMetSerGlyHisArgValLeuProLeu 160
Db 532 GTGGAGCATGGGCACATCAATCAATAGCATGTCTGSCCACCAGTGTACCCCTG 591
Qy 161 SerValThrHisPheTyrSerAlaThrLysTyrAlaValThrAlaLeuThrGluGlyLeu 180
Db 592 TCTGTGACCCACTTCTATAGTCCACCAAGATGATGCCGTCACTGGCGTGCACAGAGGACTG 651
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Qy 181 ArgGlnGluLeuArgGluAlaGlnThrHisIleArgAlaThrCysIleSerProGlyVal 200
Db |||||
Qy 652 AGCAAGAGCTTCGGAGGCCAGACCACATCCGAGCCACGTGCATCTCTCCAGGTGTG 711
Db |||||
Qy 201 ValGluThrGlnPheAlaPheLysLeuHisAspLysAspProGluLysAlaAlaAlaThr 220
Db |||||
Qy 712 GTGAGACACAATTGCGCTTCAAACTCCACGACAAAGGACCTGAGAAAGGCAGCTGCCACC 771
Db |||||
Qy 221 TyrGluGlnMetLysCysLeuLysProGluAspValAlaGluAlaValIleTyrValLeu 240
Db |||||
Qy 772 TATGAGCAAAATGAAGTGTCTCAAAACCGAGGATGTGGCCGAGGCTGTTATCTAGTCCTC 831
Db |||||
Qy 241 SerThrProAlaHisIleGlnIleGlyAspIleGlnMetArgProThrGluGlnValThr 260
Db |||||
Qy 832 AGCACCCCGCACACATCCAGATTGGAGACATCCAGATGAGGCCCCACGGAGCGGTGACC 891
Db |||||
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Search completed: September 16, 2004, 17:55:24
Job time : 429 secs

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